



ORIGIN GGMDFCHFFRTPLPPLAEMKQVQAFSLCLTTAFIYLMTRL"

Query Match 100.0%; Score 887; DB 9; Length 887;  
Best Local Similarity 100.0%; Pred. No. 5.7e-144;  
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 CGGGCCAAGAAAACGAGGAGGCGCGGCCCCCAGCAGAGGCGCGGACCATGGTTGACCA 60
DB 1 CGGGCCAAGAAAACGAGGAGGCGCGGCCCCCAGCAGAGGCGCGGACCATGGTTGACCA 60
OY 61 GTTGGGGAGGCGCACCACCATGAGCCCGCTGCGGAGCGCACCAGCTGTGTGCGC 120
DB 61 GTTGGGGAGGCGCACCACCATGAGCCCGCTGCGGAGCGCACCAGCTGTGTGCGC 120
OY 121 CGACTACCTGGGGGTACTGCGCCCGGAGAACCCCGACCCCGAGCCGCGCATCCACGCC 180
DB 121 CGACTACCTGGGGGTACTGCGCCCGGAGAACCCCGACCCCGAGCCGCGCATCCACGCC 180
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DB 181 CGAGGCGCGGCTGCTGCTCGCGCGCGCCAGGTTACGGAGATTCAACGGTCTTTT 240
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DB 241 CTCGCGCTACCTGCGCTACCCCGGAAACCGCTTGCAGCTGTGGCGCTGATGCGGATT 300
OY 301 CGTGTCTCCGACAGCCCGGCGCCCACTGGGGAGAGTGTGACGCTGTGACCTTGGC 360
DB 301 CGTGTCTCCGACAGCCCGGCGCCCACTGGGGAGAGTGTGACGCTGTGACCTTGGC 360
OY 361 AGGGAAGCTGTGAGAGAGAGGCGCGCTGTGACCGCCCGGTGAGAAATGGGGCTTCCA 420
DB 361 AGGGAAGCTGTGAGAGAGAGGCGCGCTGTGACCGCCCGGTGAGAAATGGGGCTTCCA 420
OY 421 GCCGCGGCTAAAGAGAGAGGCGCGCTGTGACCGCCCGGTGAGAAATGGGGCTTCCA 480
DB 421 GCCGCGGCTAAAGAGAGAGGCGCGCTGTGACCGCCCGGTGAGAAATGGGGCTTCCA 480
OY 481 GGTGAGCTGCGGCTGATGAGAGAGGCGCGCTGTGACCGCCCGGTGAGAAATGGGGCTTCCA 540
DB 481 GGTGAGCTGCGGCTGATGAGAGAGGCGCGCTGTGACCGCCCGGTGAGAAATGGGGCTTCCA 540
OY 541 TGGCTTTTGTCACTTCTTGAAGACCCCTTTCACGCTTTTGTGAGAAACAGTGTGT 600
DB 541 TGGCTTTTGTCACTTCTTGAAGACCCCTTTCACGCTTTTGTGAGAAACAGTGTGT 600
OY 601 CAGGCTTTTGTCACTTCTTGAAGACCCCTTTCACGCTTTTGTGAGAAACAGTGTGT 660
DB 601 CAGGCTTTTGTCACTTCTTGAAGACCCCTTTCACGCTTTTGTGAGAAACAGTGTGT 660
OY 661 ATGAGTTTAAACCTTTTAAACCGCTTTCACGCTTTTGTGAGAAACAGTGTGT 720
DB 661 ATGAGTTTAAACCTTTTAAACCGCTTTCACGCTTTTGTGAGAAACAGTGTGT 720
OY 721 ATGTGTGAGAAACAGAACTGAGGAAAGACCTTCCCAACCCAGACCTTTTATCTGA 780
DB 721 ATGTGTGAGAAACAGAACTGAGGAAAGACCTTCCCAACCCAGACCTTTTATCTGA 780
OY 781 ATGATATACAGAGAGTCTGAGGTTGATTTGGCCAGTGTGTTTAACTTGTGCAAGTACT 840
DB 781 ATGATATACAGAGAGTCTGAGGTTGATTTGGCCAGTGTGTTTAACTTGTGCAAGTACT 840
OY 841 CAGGTGTGAGCAAGAAATGCAATGCTTCTTGAAGTGAAGAA 887
DB 841 CAGGTGTGAGCAAGAAATGCAATGCTTCTTGAAGTGAAGAA 887
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RESULT 2  
LOCUS BD233466 1168 bp DNA linear PAT 17-JUL-2003  
DEFINITION Human protein having hydrophobic domain and DNA encoding the same.  
ACCESSION BD233466

VERSION BD233466.1 GI:33043236  
KEYWORDS JP 2002519016-A/12.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)

REFERENCE Kato, S. and Kimura, T.  
TITLE Human protein having hydrophobic domain and DNA encoding the same  
JOURNAL Parent: JP 2002519016-A 12 02-JUL-2002;  
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC

## COMMENT

OS Homo sapiens (human)  
PN JP 2002519016-A/12  
PD 02-JUL-2002  
PF 18-JUN-1999 JP 2000557267  
PI SRIISHI KATO, TOMOKO KIMURA  
PC C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N5/10, C12N5/00, C12N5/PC 00

CC Human protein having hydrophobic domain and DNA encoding the  
CC same  
FH Key Location/Qualifiers  
FT source 1..1168  
FT location/Qualifiers  
FT 1..1168 /organism='Homo sapiens (human)'.  
FT /mol\_type='genomic DNA'  
FT /db\_xref='taxon:9606'

## FEATURES

source

## ORIGIN

Query Match 91.6%; Score 812.4; DB 6; Length 1168;  
Best Local Similarity 99.9%; Pred. No. 4.8e-131;  
Matches 813; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 134 TACTGCGCGCGGAGAACCGGCGACCCCGAGCGCGGCGCATCCAGCGCGGAGCGCGG 193
DB 134 TACTGCGCGCGGAGAACCGGCGACCCCGAGCGCGGCGCATCCAGCGCGGAGCGCGG 193
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DB 61 TACTGCGCGCGGAGAACCGGCGACCCCGAGCGCGGCGCATCCAGCGCGGAGCGCGG 120
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DB 194 CTGCGCTCGCGCGCGCGCAGGTTACGAGAGATTCAACCGGTCTTTTCTCGCGCTACCTC 253
OY 121 CTGCGCTCGCGCGCGCGCAGGTTACGAGAGATTCAACCGGTCTTTTCTCGCGCTACCTC 180
DB 121 CTGCGCTCGCGCGCGCGCAGGTTACGAGAGATTCAACCGGTCTTTTCTCGCGCTACCTC 180
OY 254 GGTACCCCGGAGAACCGCTTGCAGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 313
DB 254 GGTACCCCGGAGAACCGCTTGCAGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 313
OY 181 GGTACCCCGGAGAACCGCTTGCAGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240
DB 181 GGTACCCCGGAGAACCGCTTGCAGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240
OY 314 AGCCCGCGCGCGCGCAGGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 373
DB 314 AGCCCGCGCGCGCGCAGGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 373
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DB 374 GAGAGAGGCGCGCTGTGATCCGCGGTGAGAAAGTGGGCTTCCAGCGCGGCTAAAG 433
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DB 301 GAGAGAGGCGCGCTGTGATCCGCGGTGAGAAAGTGGGCTTCCAGCGCGGCTAAAG 360
OY 434 GAGCAGAGAGGCGAGCTGTGCGCGGAGCTGCGACCGCTGTGTGCTTGTGAGCTGCGG 493
DB 434 GAGCAGAGAGGCGAGCTGTGCGCGGAGCTGCGACCGCTGTGTGCTTGTGAGCTGCGG 493
OY 361 GAGCAGAGAGGCGAGCTGTGCGCGGAGCTGCGACCGCTGTGTGCTTGTGAGCTGCGG 420
DB 361 GAGCAGAGAGGCGAGCTGTGCGCGGAGCTGCGACCGCTGTGTGCTTGTGAGCTGCGG 420
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DB 554 TTCTTCAAGGACCCCTTTCACCTGCTTTTGTGAGAAACAGCTGTGACAGGCTTTTCTG 613
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DB 614 TCATCTGTGTTAACAACAGCTTCAATTATCTGTGACAGATTAATGAGTTTAA 673
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Db 541 TCATGCTTTTAACAACAGCCCTTCATTATCTCTGAGACAGATTATATGATTTTAA 600  
Qy 674 CTTTAAACCGCTTACCTGCGCAACTGTGACCACTAATGACAGATGTGTGAGACA 733  
Db 601 CTTTAAACCGCTTACCTGCGCAACTGTGACCACTAATGACAGATGTGTGAGACA 660-715  
Qy 734 AGAAGTGAAGGAAAGACCTTCCCGACCCGAGAGCTTTTATCTGAATGACATACAGAA 793  
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Qy 794 GTCTGAGGTGTGTATTTGGCCAGTGTTTTAACTTTGTGACAGTACTGAGGTGTGAGAC 853  
Db 721 GTCTGAGGTGTGTATTTGGCCAGTGTTTTAACTTTGTGACAGTACTGAGGTGTGAGAC 780  
Qy 854 AGAAGTGAAGTGTCTCTCTGAGTGAAGAA 887  
Db 781 AGAAGTGAAGTGTCTCTCTGAGTGAAGAA 814

RESULT 3  
AF285092 615 bp mRNA linear PRI 08-NOV-2001  
LOCUS AF285092 Homo sapiens Bcl-2-like protein 10 mRNA, complete cds.  
DEFINITION AF285092 AF285092.1 GI:9837265  
VERSION AF285092.1 GI:9837265  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
REFERENCE 1 (bases 1 to 615)  
AUTHORS Zhang, H., Holzgreve, W. and De Geyter, C.  
TITLE Bcl-2-L-10, a novel anti-apoptotic member of the Bcl-2 family, blocks apoptosis in the mitochondria death pathway but not in the death receptor pathway  
JOURNAL Hum. Mol. Genet. 10 (21), 2329-2339 (2001)  
MEDLINE 21548034  
PUBMED 11689480  
REFERENCE 2 (bases 1 to 615)  
AUTHORS Zhang, H.H.  
TITLE Direct Submission  
JOURNAL Submitted (05-JUL-2000) University Women's Hospital, Schanzenstrasse 46, Basel 4057, Switzerland  
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source location/Qualifiers  
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ORIGIN  
Query Match 69.3%; Score 615; DB 9; Length 615;  
Best Local Similarity 100.0%; Pred. No. 8.3e-97;  
Matches 615; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 ATGGTTGACGATGGCGGAGGACGACGACATGGCCGCTGCGGAGGACGACGAG 109  
Db 1 ATGGTTGACGATGGCGGAGGACGACGACATGGCCGCTGCGGAGGACGACGAG 60  
Qy 110 CTGTTGCTGGCGGACGATCTGAGGTACTGCGCCCGGAAACCGCGGACCCCGGCGG 169  
Db 61 CTGTTGCTGGCGGACGATCTGAGGTACTGCGCCCGGAAACCGCGGACCCCGGCGG 120

Qy 170 CCATTCAGCGCCGAGAGCGCGGCTGCGCTCCGCGCGCGCAGGTTACGCGAGATTTCAC 229  
Db 121 CCATTCAGCGCCGAGAGCGCGGCTGCGCTCCGCGCGCGCAGGTTACGCGAGATTTCAC 180  
Qy 230 CGGTCTTTTTCCTCCGCTTACCTGCGCTACCCCGGAAACGCTTGTGAGCTGTGCGCTG 289  
Db 181 CGGTCTTTTTCCTCCGCTTACCTGCGCTACCCCGGAAACGCTTGTGAGCTGTGCGCTG 240  
Qy 290 ATGGCGGATTCGCGCTCTCCGACAGCCCGCGCCGACCTGCGGACAGGTGTGACGCTC 349  
Db 241 ATGGCGGATTCGCGCTCTCCGACAGCCCGCGCCGACCTGCGGACAGGTGTGACGCTC 300  
Qy 350 GTGACCTTCGCGAGGACGCTGCTGAGAGAGGCGCGCTGTGACCGCCGCTGGAAGAAG 409  
Db 301 GTGACCTTCGCGAGGACGCTGCTGAGAGAGGCGCGCTGTGACCGCCGCTGGAAGAAG 360  
Qy 410 TGGGGCTTCGACCGCGGCTTAAAGAGAGGAGGAGCGTCCCGGAGCTGCCAGCGC 469  
Db 361 TGGGGCTTCGACCGCGGCTTAAAGAGAGGAGGAGCGTCCCGGAGCTGCCAGCGC 420  
Qy 470 CTGCTGCGCTTGTGCTGAGCTCCGCGCTCATGTGGGAGAGCACCGCGCTGTGAGGCTCAG 529  
Db 421 CTGCTGCGCTTGTGCTGAGCTCCGCGCTCATGTGGGAGAGCACCGCGCTGTGAGGCTCAG 480  
Qy 530 GCGCGCTGGAGTGGCTTTTGTCACTTCTTCAGAGACCCGCTTCACATGCTTTTGGAGA 589  
Db 481 GCGCGCTGGAGTGGCTTTTGTCACTTCTTCAGAGACCCGCTTCACATGCTTTTGGAGA 540  
Qy 590 AAACAGCTGTTCAGAGCTTTTCTGTCACTTGTAAACAGAGCTTCAATTATCTCGG 649  
Db 541 AAACAGCTGTTCAGAGCTTTTCTGTCACTTGTAAACAGAGCTTCAATTATCTCGG 600  
Qy 650 ACAGATTAATATGA 664  
Db 601 ACAGATTAATATGA 615

RESULT 4  
HSA458330 585 bp DNA linear PRI 25-APR-2002  
LOCUS HSA458330 Homo sapiens NRH gene for anti-apoptotic protein.  
DEFINITION AJ458330 AJ458330.1 GI:20338765  
ACCESSION AJ458330.1 GI:20338765  
VERSION anti-apoptotic protein, NRH gene.  
KEYWORDS anti-apoptotic protein, NRH gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
REFERENCE 1  
AUTHORS Aouacheria, A., Arnaud, E., Venet, S., Lalle, P., Gouy, M., Rigal, D. and Gillet, G.  
TITLE Nrh, a human homologue of Nr-13 associates with Bcl-Xs and is an inhibitor of apoptosis  
JOURNAL Oncogene 20 (41), 5846-5855 (2001)  
MEDLINE 21472727  
PUBMED 11593390  
REFERENCE 2 (bases 1 to 585)  
AUTHORS Gillet, G.  
TITLE Direct Submission  
JOURNAL Submitted (23-APR-2002) Gillet G., Ibcip, CNRS UMR 5086, 7 PASSAGE DU VERCOIS, 69367, FRANCE  
FEATURES  
source location/Qualifiers  
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## ORIGIN

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Query Match      66.0%; Score 585; DB 9; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.3e-91;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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200 TCCCGGCGCGCAGGTTACGCGAGATTCAACCGGTCCTTTTCTCCGCTACCTCGGCTAC 259
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260 CCGCGGAAACCGGTTGAGCTGTGGCGCTGATGGGGAATCCGTGCTCTCCGACAGCCGC 319
181 CCGCGGAAACCGGTTGAGCTGTGGCGCTGATGGGGAATCCGTGCTCTCCGACAGCCGC 240
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301 GCGCGGCTGTGATCCGCCCGGTGAGAAAGTGGGGCTTCAGCGCGGCTAAAGAGCAG 360
440 GAGGGCGAGCTGTGCGCGGAGCTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTG 499
361 GAGGGCGAGCTGTGCGCGGAGCTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTG 420
500 GGGCGAGCAGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTG 559
421 GGGCGAGCAGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTG 480
560 AGGACCCCTTTCACCTGGCTTTTGAAGAAAAGCTGTGTCAGGCTTTTGTGTCATGC 619
481 AGGACCCCTTTCACCTGGCTTTTGAAGAAAAGCTGTGTCAGGCTTTTGTGTCATGC 540
620 TTGTTAACACAGGCTTCACTTATCTCTGAGACAGATTATATGA 664
541 TTGTTAACACAGGCTTCACTTATCTCTGAGACAGATTATATGA 585
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## RESULT 5

BD233456 582 bp DNA linear PAT 17-JUL-2003  
DEFINITION Human protein having hydrophobic domain and DNA encoding the same.  
ACCESSION BD233456  
VERSION BD233456.1 GI:33043226  
KEYWORDS JP 2002519016-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

## REFERENCE

AUTHORS Kato, S. and Kimura, T.  
TITLE Human protein having hydrophobic domain and DNA encoding the same  
JOURNAL Patent: JP 2002519016-A 2 02-JUL-2002;  
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC

## COMMENT

OS Homo sapiens (human)  
PN JP 2002519016-A/2  
PD 02-JUL-2002  
PP 18-JUN-1999 JP 2000557267  
PI SEISHI KATO, TOMOKO KIMURA  
PC C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N5/10, C12N5/00, C12N5/PC  
CC Human protein having hydrophobic domain and DNA encoding the  
FH source  
FT 1.582  
FT location/Qualifiers  
FT 1.582  
FT /organism="Homo sapiens (human)"

## FEATURES

source location/Qualifiers  
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## ORIGIN

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Query Match      65.6%; Score 582; DB 6; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.4e-91;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

80 ATGGCCGACCCGCTGCGGAGCGACCGAGCTGTTGCTGAGCGACTACCTGGGTTACTGC 139
1 ATGGCCGACCCGCTGCGGAGCGACCGAGCTGTTGCTGAGCGACTACCTGGGTTACTGC 60
140 GCCCGGAAACCCGACCCCGAGGCGCGCATTCAGGCCCGAGGCGCGGTGCGGC 199
61 GCCCGGAAACCCGACCCCGAGGCGCGCATTCAGGCCCGAGGCGCGGTGCGGC 120
200 TCCCGGCGCGCAGGTTACGCGAGATTCAACCGGTCCTTTTCTCCGCTACCTCGGCTAC 259
121 TCCCGGCGCGCAGGTTACGCGAGATTCAACCGGTCCTTTTCTCCGCTACCTCGGCTAC 180
260 CCGCGGAAACCGGTTGAGCTGTGGCGCTGATGGGGAATCCGTGCTCTCCGACAGCCGC 319
181 CCGCGGAAACCGGTTGAGCTGTGGCGCTGATGGGGAATCCGTGCTCTCCGACAGCCGC 240
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421 GGGCGAGCAGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTG 480
560 AGGACCCCTTTCACCTGGCTTTTGAAGAAAAGCTGTGTCAGGCTTTTGTGTCATGC 619
481 AGGACCCCTTTCACCTGGCTTTTGAAGAAAAGCTGTGTCAGGCTTTTGTGTCATGC 540
620 TTGTTAACACAGGCTTCACTTATCTCTGAGACAGATTATATGA 661
541 TTGTTAACACAGGCTTCACTTATCTCTGAGACAGATTATATGA 582
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## RESULT 6

CQ752105 726 bp DNA linear PAT 03-FEB-2004  
LOCUS CQ752105  
DEFINITION Sequence 38039 from Patent WO2068579.  
ACCESSION CQ752105  
VERSION CQ752105.1 GI:42387450  
KEYWORDS Homo sapiens (human)  
SOURCE

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL	Patent: WO 0206579-A, 38039 06-SEP-2002; PE Corporation (NY) (US)
FEATURES	Location/Qualifiers source 1..726 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
ORIGIN	
Query Match	64.8%; Score 574.4; DB 6; Length 726;
Best Local Similarity	90.2%; Pred. No. 96-90;
Matches	655; Conservative 0; Mismatches 1; Indels 70; Gaps 1
Qy	50 ATGCTTGAACCAAGTTCCGGAGGCGCACACCATGCGCCGCTGCGGAGCGCACCGAG 109
Db	1 ATGGTTGACCAAGTTCCGGAGGCGCACACCAATGCGCCGCTGCGGAGCGCACCGAG 60
Qy	110 CTGTTGCTGGGCGCACTACCTGGGGGACACGCGCCGGGAAACCGCGGACCCCGAGCGCGG 169
Db	61 CGGTTGCTGGGCGCACTACCTGGGGGACACGCGCCGGGAAACCGCGGACCCCGAGCGCGG 120
Qy	170 CCATTCACGCGCCGAGGCGCGGCTGCGCTCCGCGCGCGCACGAGTTACGCGCAATTAC 229
Db	121 CCATTCACGCGCCGAGGCGCGGCTGCGCTCCGCGCGCGCACGAGTTACGCGCAATTAC 180
Qy	230 CGGTCCTTTTCTCGGCTTACTCGGCTTACCCTCGGAAACCGCTTGAAGTGTGGCGCTG 289
Db	181 CGGTCCTTTTCTCGGCTTACTCGGCTTACCCTCGGAAACCGCTTGAAGTGTGGCGCTG 240
Qy	290 ATGGCGGATTCGAGTCTCTCGACACAGCCCGGCCCACTGGGGGACAGTGTGACGCTC 349
Db	241 ATGGCGGATTCGAGTCTCTCGACACAGCCCGGCCCACTGGGGGACAGTGTGACGCTC 300
Qy	350 GTGACCTTTCGAGGAGCGCTGTGAGAGAGGACCGCTGTGACCGCCCGGTGAAGAAG 409
Db	301 GTGACCTTTCGAGGAGCGCTGTGAGAGAGGACCGCTGTGACCGCCCGGTGAAGAAG 360
Qy	410 TGGGGCTTCCAGCCCGCGCTAAAGAGACAGAGGGCGACAGTGGCCCGGAGCTGCCAGGCG 469
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Qy	470 CTGGTGGGCTTCTGTAGAGCTCGCGGCTCAATGGGGGACGACCCGCGCTGACAGGCTCAG 529
Db	421 CTGGTGGGCTTCTGTAGAGCTCGCGGCTCAATGGGGGACGACCCGCGCTGACAGGCTCAG 480
Qy	530 GGGCGCTG----- 537
Db	481 GGGCGCTGCTGAGACACGCGCGACACCGGGACACGGGGCGGACCGGACCGGAGAG 540
Qy	538 -----GGATGGCTTTTGTGCACTTCTTCAGAGAACCCCTTTCACATGCG 579
Db	541 CGCCACGAGGCTGACGAGAGGCTTTTGTGCACTTCTTCAGAGAACCCCTTTCACATGCG 600
Qy	580 TTTTGGAGAAAACAGCTGTCTCAAGGCTTTTCTGTCAAGTCTGTAAACAACAGCCTTCAT 639
Db	601 TTTTGGAGAAAACAGCTGTCTCAAGGCTTTTCTGTCAAGTCTGTAAACAACAGCCTTCAT 660
Qy	640 TTATCTCTGGAACAAGATTATATGAGTTTAAACCTTTTAAACCGGCTTCACTGCCCCA 699
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Qy	700 CTGGA 705
Db	721 CTGGA 726

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RESULT 7
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LOCUS      AC023906      93287 bp    DNA        linear    PRI 06-JUL-2001
DEFINITION Homo sapiens chromosome 15 clone CTD-2184D3 map 15q21.2, complete
              sequence.
ACCESSION  AC023906
VERSION    AC023906
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
REFERENCE  1 (bases 1 to 93287)
AUTHORS   Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  2 (bases 1 to 93287)
AUTHORS   Burke,J., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
              Pate,D., Dore,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
              Pate,D., and Hood,L.
              Sequencing of human chromosome 15 D1S146-D1S117 region
              unpublished
REFERENCE  3 (bases 1 to 93287)
AUTHORS   Rowen,L., Madan,A., Qin,S., Abbagi,N., Baradarani,L., Birditt,B.,
              Bloom,S., Dore,M., Dichtoff,R., Fleetwood,P., Harrison,G.,
              James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.,
              and Hood,L.
              Direct Submission
              Submitted (20-FEB-2000) Multimegabase Sequencing Center, University
              of Washington, PO Box 357730, Seattle, WA 98195, USA
REFERENCE  3 (bases 1 to 93287)
AUTHORS   Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
              Burke,J., Dore,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
              Pate,D., and Hood,L.
              Direct Submission
              Submitted (04-JUL-2001) Multimegabase Sequencing Center, Institute
              for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
              98105, USA
REFERENCE  4 (bases 1 to 93287)
AUTHORS   Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
              Burke,J., Dore,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
              Pate,D., and Hood,L.
              Direct Submission
              Submitted (06-JUL-2001) Multimegabase Sequencing Center, Institute
              for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
              98105, USA
COMMENT    On Jul 4, 2001 this sequence version replaced gi:12248292.
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              Genome Center
              Center: Multimegabase Sequencing Center
              Center code: UMMS
              Web site: http://chroma.mbc.washington.edu/meg_www
              Contact: leerowens@systemsbiology.org
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              Summary Statistics
              Sequencing vector: pUC18; 108752
              Chemistry: Dye-terminator Big Dye; 90% of reads
              Chemistry: Dye-Primer Big Dye; 10% of reads
              Assembly program: Phrap; version 0.990399
Note: Data from overlapping BACs AC01674 [drafting center:
UMMSC], AC090970 [drafting center: UMMS], and AC016824 [drafting
center: CTC] was added for finishing
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possible"
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misc_feature

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14722.	.14808
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QY	61 GTTGGGGGAGGCGCACACATGCTCGACCCGCTGCGGAGGCGACCGAGCTGTTGCTGGC 120
Db	64931 GTTGGGGGAGGCGCACACATGCTCGACCCGCTGCGGAGGCGACCGAGCTGTTGCTGGC 64872
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Db	64871 CGACTACCTGGGGGATCTGCGCCCGGGGAAACCGGACCCCGAGACCCGCGGCATCCACAGCC 64812
QY	181 CGAGGCGCGCGTGTGTGGCTCCGCGGCGCGCAGGTTACGACGATTCACCGATCTTTT 240
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QY	241 CTCGCGCTACTCTCGGCTAACCCCGGGAAACCGCTTGAGCTGTGGCGCTGATGGCGGATTC 300
Db	64751 CTCGCGCTACTCTCGGCTAACCCCGGGAAACCGCTTGAGCTGTGGCGCTGATGGCGGATTC 64692
QY	301 CGTGCCTCCGACAGGCCCCCGGCCCACTTGGGGAGAGTGTGACGCTGTGACCTTTGCG 360
Db	64691 CGTGCCTCCGACAGGCCCCCGGCCCACTTGGGGAGAGTGTGACGCTGTGACCTTTGCG 64632
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QY	421 GCCGCGGCTAAAGAGAGAGAGGGCGTGTGCCCGGGACTGTCCAGCGCTGTGTGACCTT 480
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QY	481 GCTGAGCTTCGGGCTCATGTGGGGCGACCCGCGCTGTGCTCAAGCTCAAGGCGGCTGGGA 540
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DEFINITION	Homo sapiens chromosome 15 clone RP11-337B11 map 15q21, LOW-PASS
SEQUENCE SAMPLING.	
ACCESSION	AC018903
VERSION	AC018903.2 GI:8247797
KEYWORDS	HTG; HTGS PHASE0.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	TITLE
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.	
1 (bases 1 to 214669)	
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradaran, L., Birditt, B.,	
Bloom, S., Doris, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A.,	
Madan, A., Nesbitt, R., Shaffer, T. and Hood, L.	
Sequencing of human chromosome 15 D15S146-D15S117 region	
Unpublished	
2 (bases 1 to 214669)	
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradaran, L., Birditt, B.,	
Bloom, S., Doris, M., Dickhoff, R., Fleetwood, P., Harrison, G.,	
Kaur, A., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T.	
and Hood, L.	
Direct Submission	
Submitted (22-DEC-1999) Multimegabase Sequencing Center, University	
of Washington, PO BOX 357730, Seattle, WA 98195, USA	
On Jun 4, 2000 this sequence version replaced g1.6630517.	
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Genome Center	
Center: Multimegabase Sequencing Center	
Center code: UWMSC	
Web site: http://chroma.mbt.washington.edu/mcg_www	
Contact: leerowens@systembiology.org	
Summary Statistics	
Sequencing vector: pUC18, 108752	
Chemistry: Dye-terminator Big Dye; 90% of reads	
Chemistry: Dye-primer Big Dye; 10% of reads	
Assembly program: Phrap; version 0.990399	
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* NOTE: This record contains 192 individual	
* sequencing reads that have not been assembled into	
* contigs. Runs of N are used to separate the reads	
* and the order in which they appear is completely	
* arbitrary. Low-pass sequence sampling is useful for	
* identifying clones that may be gene-rich and allows	
* overlap relationships among clones to be deduced.	
* However, it should not be assumed that this clone	
* will be sequenced to completion. In the event that	
* the record is updated, the accession number will	
* be preserved.	
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807	906: gap of unknown length
907	2068: contig of 1162 bp in length
2069	2169: gap of unknown length
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4385	5201: contig of 817 bp in length
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5302	6544: contig of 1243 bp in length
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6645	7472: contig of 828 bp in length
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 QY 776 TCTGAATGCAATCAAGAGGCTTCTGAGGAGGATTTGGCCAGTGTTTAACTTGACAA 835  
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SOURCE  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
COMMENT

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Homo sapiens chromosome 15 clone RP11-337B11 map 15q21, LOW-PASS  
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AC018903.2 GI:8247797  
HTG: HTGS PHASE0.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 214669)  
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradaran, L., Birditt, B.,  
Madan, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A.,  
Madan, A., Nesbitt, R., Shaffer, T., and Hood, L.  
Sequencing of human chromosome 15 D15S146-D15S117 region  
Unpublished  
2 (bases 1 to 214669)  
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradaran, L., Birditt, B.,  
Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G.,  
James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T.,  
and Hood, L.  
Direct Submission  
Submitted (22-DEC-1999) Multimegabase Sequencing Center, University  
of Washington, PO BOX 357730, Seattle, WA 98195, USA  
On Jun 4, 2000 this sequence version replaced gi:630517.  
----- Genome Center  
Center: Multimegabase Sequencing Center  
Center code: UMMSC  
Web site: [http://chroma.mbt.washington.edu/msg\\_www](http://chroma.mbt.washington.edu/msg_www)  
Contact: [leerowen@systemsbiology.org](mailto:leerowen@systemsbiology.org)  
----- Summary Statistics  
Sequencing vector: pUC18; L08752  
Chemistry: Dye-terminator Big Dye; 90% of reads  
Chemistry: Dye-Primer Big Dye; 10% of reads  
Assembly program: Phrap; version 0.990399  
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\* NOTE: This record contains 192 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
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907 906: gap of unknown length  
2069 2068: contig of 1162 bp in length  
2169 2168: gap of unknown length  
3021 3020: contig of 852 bp in length  
3121 3120: gap of unknown length  
4284 4284: contig of 1164 bp in length  
4285 4284: gap of unknown length  
4385 5201: contig of 817 bp in length  
5202 5201: gap of unknown length  
5302 6544: contig of 1243 bp in length  
6545 6544: gap of unknown length  
6645 7472: contig of 828 bp in length  
7473 7472: gap of unknown length  
7573 7576: contig of 1184 bp in length  
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8857 8856: gap of unknown length  
9658 9658: gap of unknown length  
9758 9758: gap of unknown length  
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10906 11005: gap of unknown length  
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14312 15465: contig of 1154 bp in length  
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15566 16379: contig of 814 bp in length  
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17625 17724: gap of unknown length  
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19775 19874: gap of unknown length  
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22037 22136: gap of unknown length  
22137 23023: contig of 887 bp in length  
23024 23123: gap of unknown length  
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26386 26485: gap of unknown length  
26486 27325: contig of 840 bp in length  
27326 27425: gap of unknown length  
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39727 39826: gap of unknown length  
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*	64129:	64228: gap of unknown length
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*	68426:	68525: gap of unknown length
*	68526:	69322: contig of 797 bp in length
*	69323:	69422: gap of unknown length
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*	80775:	80874: gap of unknown length
*	80875:	81590: contig of 816 bp in length
*	81691:	81790: gap of unknown length
*	81791:	82928: contig of 1138 bp in length
*	82929:	83028: gap of unknown length
*	83029:	83032: contig of 874 bp in length
*	83903:	84002: gap of unknown length
*	84003:	85193: contig of 1191 bp in length
*	85194:	85293: gap of unknown length
*	85294:	86149: contig of 856 bp in length

Db	93333	CGACTACTGTAAGTAACTGCGCCCCGGGAAACTGGACCCCCGAGCGGAGGCATTACAC	93392
QY	180	CCGAGGCCGCCGCTGCTGCGCTCCGCGGCGCCAGGTTTAGGCAAGATTACCCGCTCTTTT	239
Db	93393	CCGAGGCCGCCGCGAGCTTGGCTCCGCAAGCCGCAAGGTTACGGCAATTCACCGCTCTTTT	93452
QY	240	TTCTCCGCTTACCTCGGCTACCCCGGGAAACCGCTTGAGCTGGGCGGCTGATGGCGATT	299
Db	93453	TTCTCCCTTACCTCGGATACCCGAAACCGCTTGACCTGGGCGGCTGATGGCGATT	93512
QY	300	CCGCTCTCTCGGACAGCGCCGCGGCCCAACTGGGGGAGAGTGGTGAAGCTCGTGAACCTTTCG	359
Db	93513	CCGCTACTCTCGACAGACCCTGCGCCACTAGGGCAAAAAGGGAGACGCTCGTGAACCTTTC	93572
QY	360	CAGGAGCGCTTGAGAGAGGGCGCTGCTGAACCGCCGCTGGAGAAAGTGGGCTTCC	419
Db	93573	CAGGAGCACTTCTTGAGAAAAGGCCCTGATGAACCCCCCTTGAAAAAAATAGCTTTC	93632
QY	420	AGCGCGCGCTAAAGAGACAGAGAGGGGAGCGTGGCCCGGGACTGSCCAGCGCTGTGGCTT	479
Db	93633	AAACCCCGGCTAAAGAACAAAGAGAGCACTGGCGCC-AGACTGGCCAAACCTGGAGACCT	93691
QY	480	TGCTGAGCTGCGGCGTCAATGGG	501
Db	93692	TACTGAACCTAGAACTTAATGG	93713

RESULT 10					
BV209090					
LOCUS	BV209090	456 bp	DNA	linear	STS 02-SEP-2004
DEFINITION	BC12L10.1137 Rhesus macaque genomic DNA				
ACCESSION	clone MFA137, sequence tagged site.				
VERSION	BV209090.1	GI:51853634			

SOURCE ORGANISM	Macaca mulatta (rhesus monkey, Macaca mulatta)
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100	100

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopitheciinae; Macaca.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 456)	Spindel, E.R., Pauley, M., Jia, Y., Boyle, N., Jiang, S., Gravett, C., Lupo, S.L., Ali, H., Ojeda, S.R. and Norgren, R.B.	Targeted amplification of the 3' end of rhesus macaque orthologs of

JOURNAL  
COMMENT  
Unpublished (2004)

**Contact: Spindel ER**  
**Division of Neuroscience**  
**Oregon National Primate Research Center**  
**505 NW 185th Avenue, Beaverton, OR 97006, USA**

Tel: 403-690-5388  
Fax: 503-690-5384  
Email: [spindel@oahu.hawaii.edu](mailto:spindel@oahu.hawaii.edu)  
Primer A: TTTCTCAGCTCTTCAGGAC  
Primer B: CAGCTTTAAATTGTCAGCA  
STS size: 456  
PCR Profile:

protocol1:

Hot Start:	95 degrees C for 2.00 min
Denaturation:	95 degrees C for 0.50 min
Annealing:	51 degrees C for 0.50 min
Polymerization:	72 degrees C for 1.00 min
PCR Cycles:	35
Extension	72 degrees C for 7.0 min
Thermal Cycler:	MJ Instruments PTC100

Template:	200 ng
Primer:	each 1uM
dNTP's:	each 200 uM
Taq Polymerase:	0.05 units/ul (Fast Start High Fidelity, Roche)
Total Vol:	50 ul

## Buffer:

MgCl<sub>2</sub>: 1.8 mM  
Fast Start polymerase reaction buffer (Roche)

Bases 1-321 are 95% homologous (Blast) to bases 566-886 of NM\_020396.2. Primers were chosen to amplify genomic DNA in the 3' region of BCL2L10. As human sequence was used to design the primers, the primer sequences are not included in the rhesus sequence provided below. To obtain additional information regarding primers or clones contact: Dr. Robert Norgren, Dept of Genetics, Cell Biology & Anatomy, University of Nebraska Medical Center, 966395 Nebraska Medical Center, Omaha, NE 68198. Email: rnorgren@unmc.edu

A database containing sequences associated with this project can be found at: <http://rhesusgenecchip.unomaha.edu/index.html>.

## FEATURES

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/organism="Macaca mulatta"  
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/note="Organ: Liver; Vector: pGEM-T Easy; V-type: Plasmid; cDNA amplified from rhesus genomic DNA with the human forward and reverse primers listed above and subcloned into pGEM-T Easy."  
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## ORIGIN

## STS

## gene

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Matches 305; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db 1 CCGTTTCCAGTGGCTTTTGGAGAAACAGCGTCCAGGCTTTCTGTCAAGCTTTGTA 60  
OY 626 ACAACAGGCTTCATTATCTCTGACACAGATTATATGATTTTAACTTTTAAACCGC 685  
Db 61 GCAACAGGCTTCGTTATCTCTGACACAGATTATATGATTTTAACTTTTAAACCGC 120  
OY 686 TTCTACCTGCGCACTGTGACCACTAATGACAGATGTGTGAGAACAAAGACTGAGGA 745  
Db 121 TTCTACCTGCGCACTGTGACCACTAATGACAGATGTGTGAGAACAAAGACTGAGGA 180  
OY 746 AAGCAGCTTCCGCCACCCCAAGCGTTTATCTGAATGATPACAGAGATCCCTGAGGTGG 805  
Db 181 AAGCAGCTTCCGCCACCCCAAGCGTTTATCTGAATGATPACAGAGATCCCTGAGGTGG 240  
OY 806 TGATTGGCCAGTGTGTTTAACTTGTGACAAGTACTCAGGTGTGAGAGCAAGATCAAT 865  
Db 241 TGATTGGCCAGTGTGTTTAACTTGTGACAAGTACTCAGGTGTGAGAGCAAGATCAAT 300  
OY 866 GGCTCTTCTCTGAGTGAAGA 886  
Db 301 GGCTCTTCTCTGAGTGAAGA 321

## RESULT 11

AF102501 AF102501 1209 bp mRNA linear ROD 21-JAN-1999  
LOCUS Mus musculus Bcl-2 homolog (Bcl-2) mRNA, complete cds.  
DEFINITION  
ACCESSION AF102501  
VERSION AF102501.1 GI:4165137  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
1 (bases 1 to 1209)  
AUTHORS Song,Q., Kuang,Y., Dixit,V.M. and Vincenz,C.  
TITLE Bcl-2, a novel negative regulator of cell death, interacts with

JOURNAL EMBO J. 18 (1), 167-178 (1999)  
MEDLINE 99094902  
PUBMED 9878060  
REFERENCE 2 (bases 1 to 1209)  
AUTHORS Song,Q.Z., Kuang,Y.P., Dixit,V.M. and Vincenz,C.  
TITLE Direct Submission  
JOURNAL Submitted (28-Oct-1998) Pathology, University of Michigan, 1301 Catherine Road, Ann Arbor, MI 48109, USA

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## gene

## CDS

## ORIGIN

Query Match 29.2%; Score 259.2; DB 10; Length 1209;  
Best Local Similarity 63.1%; Pred. No. 3.8e-35;  
Matches 477; Conservative 0; Mismatches 253; Indels 26; Gaps 4;

OY 86 GACCCGCTGCGGAGACCGCAAGCTGTGTGCGCCGACTACCTGCGGCTCGCCGCG 145  
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OY 146 GAACCCGCGACCCCGAGCGCGGCGCATCAAGCCCGAGCGCGGCTGCGGCTCGCG 205  
Db 192 GAACCCGCGACCCCGAGCGCGGCGCATCAAGCCCGAGCGCGGCTGCGGCTCGCG 251  
OY 206 GCCGCAAGTTCAGGCAAGTTCACCGGCTCTTTCTCCGCTACCTGCGGCTACCCGCG 265  
Db 252 ACTAGGCAAGTTCAGGCAAGTTCACCGGCTCTTTCTCCGCTACCTGCGGCTACCCGCG 311  
OY 266 AACCGCTTCAGCTGTGTGCGCGCTGATGCGGATTCGCTCTCCGACAGCCCGCGCC 325  
Db 312 AATGCGCTTCAGCTGTGTGCGCGCTGATGCGGATTCGCTCTCCGACAGCCCGCGCC 371  
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Db 372 AGCTGAGCGCAAGTGTGATCTCTGCGCTCGGAGAGAGCTGTGAGAGAGGCGCGCT 431  
OY 386 CTGTGACCGCGCGGAGAGAGTGTGAGCTTCCAGCCGCTAAGAGAGAGAGGCG 445  
Db 432 TACATGCTGTTCAG 473  
OY 446 GACGTCGCGCGGAGAGCTGCGAGCGCGCTGTGCTGCTGAGCTGCGGCTCATGGGCG 502  
Db 474 ATAGTACCGCGGAGAGCTGCTGTCTCATGTGTAATCTGTGTAATCTGTGAGGCGGT 533  
OY 503 CAGACCGCGCGCTGCGGCTGAGGCTCAGGCGGCGCTGAGAGAGCTTTTGTCACTTCTGAG 562  
Db 534 CAGACCGCGCGCTGAGGCTTCTGCGGCTGAGGAGGCTTTTGTCCGCTTCTTCAAG 593

Qy 563 ACCCCCTTTCAGCTGGCTTTTGGAGAAAACAGTGTCTCAGGCTTTTCTGTCAAGCTTG 622  
 Db 594 AATCCTTACCGCTCGGCTTCTGGAGAGATTTGCTGATTCAGGCTTTTCTGTCAAGCTTG 653  
 Qy 623 TTACCAACAGCTTCAATTATCTCTGACAGCATTAATATGAGTTTAAACCTTTAAACC 682  
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 Db 770 CTGAGGAAGTCTCCAGGCTTGAAGACATTTCTACCTGATGC-TACATGAGATTCTGGGT 828  
 Qy 803 TGTGATTTGGCCAGTGTTTTAACTTGTGACAAAGTA 838  
 Db 829 TTGTATGGGGCCAGCATTTGAAAGGGCCCATGTA 864

## RESULT 12

AF067660 1225 bp mRNA linear ROD 04-DEC-1998  
 LOCUS Mus musculus Bcl-2 homolog (Diva) mRNA, complete cds.  
 DEFINITION AF067660  
 ACCESSION AF067660.1 GI:3955265  
 VERSION  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1225)  
 AUTHORS Inohara, N., Goulety, T. S., Carrio, R., Muniz, M., Merino, J., Garcia, I., Koseki, T., Hu, Y., Chen, S. and Nunez, G.  
 TITLE Diva, a Bcl-2 homologue that binds directly to Apaf-1 and induces BH3-independent cell death  
 JOURNAL J. Biol. Chem. 273 (49), 32479-32486 (1998)  
 MEDLINE 99047617  
 PUBMED 9829980  
 REFERENCE 2 (bases 1 to 1225)  
 AUTHORS Inohara, N. and Nunez, G.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-MAY-1998) Department of Pathology, University of Michigan Medical School, 1500 E. Medical Dr., Ann Arbor, MI 48109, USA

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 Best local similarity 29.2%; Score 259.2; DB 10; Length 1225;  
 63.1%; Pred. No. 3.8e-35;

Matches 477; Conservative 0; Mismatches 253; Indels 26; Gaps 4;  
 Qy 86 GACCCGTCGGGAGCGCACGAGCTGTGGCGCCGCTACCTGGGGTACTGGCCCGG 145  
 Db 158 GACCCACTGACAGACGACATGACAGGCTGTCTGTCTCAATATTTCTTGGGCAAG 217  
 Qy 146 GAACCCGACACCCCGAGCCGCAATCCAGCCGAGGCGGCGTCTGCTCCGCG 205  
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 Db 796 CTGAGGAAGTCTCCAGGCTTGAAGACATTTCTACCTGATGC-TACATGAGATTCTGGGT 854  
 Qy 803 TGTGATTTGGCCAGTGTTTTAACTTGTGACAAAGTA 838  
 Db 855 TTGTATGGGGCCAGCATTTGAAAGGGCCCATGTA 890

## RESULT 13

BC052690 1257 bp mRNA linear ROD 08-OCT-2003  
 LOCUS Mus musculus Bcl2-like 10, mRNA (CDNA clone MGC:60542  
 DEFINITION IMAGE:30052580), complete cds.  
 ACCESSION BC052690  
 VERSION BC052690.1 GI:30851238  
 KEYWORDS MGC.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1257)  
 AUTHORS Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heide, F., Datchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schiezer, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wotley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, X., Gibbs, R.A., Vallatou, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Faltson, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Scherch, A., Schein, J.R., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNALS  
MELNIB  
PUBMED  
22388257  
12477932  
2 (bases 1 to 1257)  
Strausberg, R.  
Direct Submission  
Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [gcgaps-remail.nih.gov](mailto:gcgaps-remail.nih.gov)  
Tissue Procurement: Minoru Ko  
cDNA Library Preparation: Yulan Piao and Minoru Ko (National Institute on Aging, NIH: <http://lgsun.grc.nia.nih.gov/cDNA/>)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooke, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantirip, S., Thomas, P.J., Touchman, J.W., Tsourgou, C., Vogt, J.L., Walker, M.A., Weherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAC Plate: 112 Row: h Column: 18  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7304926.

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FEATURES  
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ORIGIN  
Query Match 29.0%; Score 257.6; DB 10; Length 1257;  
Best Local Similarity 63.0%; Pred. No. 7.1e-35;  
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622 AATCGTTTACCGCTGCGGCTTGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGCT 681  
623 TTAAACAACGCTTATTTATCTTGTGACAGGATTTATGAGTTTAACTTTTAAAC 682  
682 TTTCACAACGCACTTTTATTTATTTGAGAAAGTTTATTTTAAAGTTTAAAG 737  
683 CGCTTACCGGCGCACTGAGCACTAATAATGAGATGTCGAGAACAGAACTGAG 742  
738 CGATCTTACCTTACCTTACCTTGAACCTCTAGAGAACATTTCTGGGTAATGATGAG 797  
743 GAAAGACCTTCCCGACCCGACCGCTTTTATCTGAAATGATGATGATGATGATGATG 802  
798 CTGAGGAAGCTCTCAAGCTTGAAGACATTTCTACTGATGCTGATGCTGATGCTG 856  
803 TGTGATTTGGCGAGTGTGTTTAACTTGTGACAGTA 838  
857 TTGTGATGCGGCGAGCAATTTGAAAGGAGGCGCATGTA 892

RESULT 14  
AY029163  
LOCUS AY029163 1074 bp mRNA linear ROD 19-JUN-2003

FEATURES	Location/Qualifiers
source	1. .1074

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/gene="Bcl2l10"  
/note="Boo, Dìva"
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**ORIGIN**

80 ATGGCCGACCCGCTGCGGAGACCCACCGACTTGTCTGCGCCGACTACTGGGGTACTTC 139

80 ATGCCGACCCGCTGCGGAGCGCACCGAGCTGTTGCTGGCCGACTACTGGGTACTGC 139

Db 12 ATGGGTGACCCGCTGCAGGATCGCACTAGACGGCTGCTGACTGACTACATATTGTTCTGC 71

140 GCCCGGAACCCGGCACCCCGAGCCGGCGCATCCACGCCCGAGCGCCGCTGCC 199

Db 72 GCACGGGGCCGAACACCCCTGAGCCACTGCCACGTCCTGTTGAGGGCGCCTTGCTGCC 131

200 TCCGCGCCGACGATTACCGCAGATTCACCGGTCTTTCTCCGCCCTACCTGGCTAC 259

Db 132 TCTGTACTAGTCAGATCCAA CAGAGCA CAGGATCTTTCAACTCCTCCGCGACTAC 191

260 CCGGGAACCGCTTCGAGCTGTGGCGCTGATGGCGATTCCGTCTCCGACAGCCCC 319

Db 192 CAGGCAACCGCCTGAGCTGTGACACAGATGGCGATGAGTTGCTCTCCAATGACCA 251

320 GGCCCACTGGGCAAGTGTGACGCTCGTACCTTCGACGGACGCTGTGAGAGA 379

Db 252 GAGTTCAACTGGGCGCCTGTGATGCTCCTGGCCTTCGTGGGACGCTATGAACCA 311

380 GGGCCGCTGTGACCGCCGGTGGAAGAGTGGGCTTCAGCCGGCTTAAGGAGCAG 439

Db 312 GACAGGACTGTTAAGCGGAGGAGGATCAAGAACCCTCTCTAC----- 357

440 GAGGCGACGTCGCCCGGACTGCCAGCGCCCTGGTGCCCTTGAGCTCGCGGCTCATG 499

AC133947

**DEFINITION** Mus musculus chromosome 9 clone RP24-189I2, complete sequence.

VERSION AC133947.3 GT:51921460

SOURCE Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 168997)

TITLE The sequence of Mus musculus clone

REFERENCE 2 (bases 1 to 168997)

TITLE	Direct Submission
-------	-------------------

Parkway, St. Louis, MO 63108, USA

**AUTHORS**      **Wilson, R.K.**

**JOURNAL Submitted (10-JUL-2004) Genome Sequencing Center, 4444 Forest Park**

REFERENCE 4 (bases 1 to 168997)

TITLE	Direct Submission

Parkway, St. Louis, MO 63108, USA

Center: Washington University Genome Sequencing Center

Web site: <http://genome.wustl.edu>

```
----- Project Information -----
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.....

source 1. .168997

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/mol_type="genomic DNA"
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/chromosome="9"
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ORIGIN

```
/clone="RP24-189I2"
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Query Match	Score	DB	Length
16.6%;	147;	10;	168997;

Best local similarity 61.54; PRed. NO. 1.45-16;  
Matches 281; Conservative 0; Mismatches 155; Indels 21; Gaps 2;

OY	86	AACCCGCTGCGGGAGGACCCAGCTGTTCGCGCGAATACCTGAGGGTAATCGCCCG	145
Db	166427	GACCCACTGCATGAAOGCATAGACGGCTGTCTGTGATACATATCTTCTCGCACGG	166486
OY	146	GAACCCGGGACCCCGGAGCTCGGGGCGCATCAAGCCCGAGGCGCGCTGCTCGCTCCGCG	205
Db	166487	GAGCCCGGACACCCCGAGAGCCACCGCCCAAGTCTGTGTGAGGCGGCGCTTGCTCGCTGTG	166546
OY	286	GCGCGCAGGTTACGGCAGATTACCGCGTCTTTTCTTCGCGCTACCTCGGCTACCCCGGG	265
Db	166547	ACTAGGCAGATCAGACGAGGACCAAGAATTTTCTTCCTCTTCTGCGAAGCCGGGGC	166606
OY	266	AACCGCTTCGAGCTGTGCGGCTGTATGCGCGAATCCGTCCTCTCCGACAGCCCGGCGCC	325
Db	166607	AATCGCTGAGACTGCTGTGAAAAGATGCGAGATAGTTGCTCTCGAAGACCAAGACTTC	166666
OY	326	ACCTGGGGCAGAGTGTGTACGCTCTGTGACCTTCGACGGGACCGTCTCTGAGAGAGGGCCG	385
Db	166667	AGCTGAGCGCACTGGTAGTGTCTCCGGCTTCGCGGGACCGTTATGAAATCAAGGCCCT	166726
OY	386	CTGTGTGACCGCCCGGTGGAAGAAGTGGGGCTTCGACCGCGCTGAAGAAGGACGAGGGC	445
Db	166727	TACATGGCTGTCAAGCAGAAAG-----GGATTCGGGGAAATCGTGT	166788
OY	446	GACGTGCGCGGGACTGCGACGCGCTGTGTGGCTTGTGACTCGCGGCTCATGGGG---	502
Db	166749	ATAGTGAACCCGAGACTGTGTCTCATATGAACTTCTGTATATCTGCTCATGGGGCGT	166828
OY	503	CAGCACCGGCGCTGGCTGAGGGCTCAAGGGGCGGTGGG	539
Db	166829	CGGCAACCGCGCAGGCTGAGGGCTCTCGCGGGCTGGG	166865

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Search completed: June 7, 2005, 21:57:49
Job time : 6833.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2005, 08:53:44 ; Search time 867.812 Seconds  
(without alignments)  
6050.630 Million cell updates/sec

Title: US-10-071-174A-1

Perfect score: 887

Sequence: 1 cgggccaagaacaccagcga.....ctctccttgagcgaagaa 887

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

1: N\_Geneseq\_16Dec04:\*  
2: geneseqn1980s:\*  
3: geneseqn1990s:\*  
4: geneseqn2000s:\*  
5: geneseqn2001as:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887	100.0	887	6	AAD46683 Human Bcl
2	812.4	91.6	1168	3	AAZ90049 Aaz90049 Hydrophob
3	582	65.6	582	3	AAZ90039 Aaz90039 Hydrophob
4	506.8	57.1	522	4	AAH47022 Aah47022 Human Bcl
5	457.2	51.5	548	4	ABK41913 Abk41913 CDNA enco
6	457.2	51.5	548	9	ADB59580 Adb59580 Connectiv
7	324.6	36.6	874	6	ABQ44404 Abq44404 Oligonuc
8	324.6	36.6	874	6	ABQ44405 Abq44405 Oligonuc
9	320	36.1	874	6	ABQ44403 Abq44403 Oligonuc
10	320	36.1	874	6	ABQ44402 Abq44402 Oligonuc
11	240.2	27.1	650	10	ADD34132 Add34132 Mouse mit
12	154	17.4	835	10	ADD34582 Add34582 Mouse mit
13	88.6	10.0	338	10	ADD34583 Add34583 Mouse mit
14	68	7.7	2000	8	ADA71938 Ada71938 Rice gene
15	60	6.8	60	6	ABN42801 Abn42801 Human spl
16	59.4	6.7	11955	2	AAK53491 Aak53491 Human ade
17	57.4	6.5	9222	8	AAI61171 Aai61171 Actinosyn
18	57.4	6.5	39949	12	ADF31997 Adf31997 Full leng
19	57.4	6.5	48200	12	ADF31998 Adf31998 Coemid 2A
20	57.4	6.5	82746	8	AAI61224 Aai61224 Actinosyn

21	56	6.3	536	10	ADB68842	Adb68842	Minority
22	55.6	6.3	1765	5	AA83822	Aa83822	DNA encod
23	55.6	6.3	1956	5	AA873207	Aa873207	DNA encod
24	55.6	6.3	1956	5	AA883791	Aa883791	DNA encod
25	55.6	6.3	3808	10	AD121903	Ad121903	Novel hum
26	55.6	6.3	4023	13	ADRO6595	Adro6595	Full len
27	55.2	6.2	3158	6	AAI50615	Aai50615	Human glu
28	52.4	5.9	9975	8	AAI61173	Aai61173	Actinosyn
29	51.8	5.8	113193	8	AAI54645	Aai54645	Streptomy
30	51.4	5.8	1293	12	ADG98245	Adg98245	Acyl-spe
31	51.4	5.8	73882	13	AD873531	Ad873531	tcp gene
32	51	5.7	58857	3	AAA58471	Aaa58471	Nucleotid
33	50.6	5.7	1437	8	ADA69472	Ada69472	Rice gene
34	50.6	5.7	14055	8	AAI61170	Aai61170	Actinosyn
35	50.4	5.7	114955	2	AAK53491	Aak53491	Human ade
36	50.2	5.7	834	10	ADK57446	Adk57446	Plant DNA
37	49.8	5.6	1194	8	ABX56038	Abx56038	M. echino
38	49.4	5.6	3540	12	AD085407	Ado85407	Streptomy
39	49.4	5.6	4440	12	AD085409	Ado85409	Streptomy
40	49.4	5.6	4860	12	AD085408	Ado85408	Streptomy
41	49.2	5.5	6200	8	ACA27156	Aca27156	Prokaryot
42	49	5.5	11100	10	AD123891	Ad123891	Streptomy
43	49	5.5	13315	10	AD123887	Ad123887	Streptomy
44	48.8	5.5	27541	4	AAI17185	Aai17185	Streptomy
45	48.8	5.5	125401	4	AAI17186	Aai17186	Streptomy

# ALIGNMENTS

RESULT 1	
ID	AAD46683 standard; DNA; 887 BP.
XX	
XX	AAD46683;
DT	27-JAN-2003 (first entry)
XX	
DE	Human Bcl-B DNA.
XX	
KW	Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder;
KW	proliferative disorder; muscle degeneration; Alzheimer's disease; CJD;
KW	Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic;
KW	Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia;
KW	SCA; dentatorubropallidoluysian atrophy; DDP4; Kennedy's disease;
KW	stroke; ischaemia; head trauma; neoplasia; anticonvulsant; vulnerable;
KW	nocturnal; neuroprotective; cytosolic; immunosuppressive; vasotropic;
KW	cerebroprotective; autoimmune disorder; chromosome 15; gene; db.
XX	
OS	Homo sapiens.
XX	
FH	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	50..664
FT	/*tag= a
FT	/product= "Human Bcl-B protein"
XX	
XX	WO200272601-A2.
XX	19-SEP-2002.
XX	07-FEB-2002; 2002WO-US003547.
XX	07-FEB-2001; 2001US-0267166P.
XX	07-FEB-2002; 2002US-00071174.
XX	(BURN-) BURNHAM INST.
XX	Reed JC, Ke N, Godzik A;
XX	WPI; 2002-723312/78.
DR	P-PSDB; AAE29097.
XX	
PT	New isolated or recombinant Bcl-B nucleic acids and polypeptides, for



CC activity; haemostatic and thrombolytic activity (e.g. treating  
 CC haemophilias); receptor/ligand activity; anti-inflammatory activity; and  
 CC tumour inhibition activity. The polynucleotides are also stated to be  
 CC useful for gene therapy. Other activities include inhibiting infections  
 CC caused by bacteria, fungi, viruses and other parasites (e.g. Hepatitis,  
 CC malaria); effecting bodily characteristics such as, e.g. weight, colour,  
 CC skin, effecting biorhythms or cardiac cycles; enhancing fertility;  
 CC treatment of depression; treatment of pain; hormonal or endocrine  
 CC activity. The polynucleotides may also be used for recombinant expression  
 CC of the protein

XX Sequence 1168 BP; 276 A; 312 C; 300 G; 280 T; 0 U; 0 Other;

SO Query Match 91.6%; Score 812.4; DB 3; Length 1168;

Best Local Similarity 99.9%; Pred. No. 7.1e-173;

Matches 813; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 74 ACCACATGCGCAGCCGCTCGGGAGCCGACCGAGCTGTGTCTGCGGCTACCTGAGG 133

DB 1 ACCACATGCGCAGCCGCTCGGGAGCCGACCGAGCTGTGTCTGCGGCTACCTGAGG 60

QY 134 TACTGCGCGCGGAAACCGGCAACCGCGCGCATCCAGCCGAGCGCGCTG 193

DB 61 TACTGCGCGCGGAAACCGGCAACCGCGCGCATCCAGCCGAGCGCGCTG 120

QY 194 CTGCGCTCCGCGCGCGAGGTTACGCGAGTTACACCGGCTCTTCTCCGCTTACCTC 253

DB 121 CTGCGCTCCGCGCGCGAGGTTACGCGAGTTACACCGGCTCTTCTCCGCTTACCTC 180

QY 254 GGTACACCGCGGAAACCGCTTGCAGCTGTGTGCGCTGATGCGGATTCCTGCTCCGAC 313

DB 181 GGTACACCGCGGAAACCGCTTGCAGCTGTGTGCGCTGATGCGGATTCCTGCTCCGAC 240

QY 314 AGCCCGCGCCACCTGCGGCGAGTGTGACGCTCGTACCTTGCAGGAGACCGTGTG 373

DB 241 AGCCCGCGCCACCTGCGGCGAGTGTGACGCTCGTACCTTGCAGGAGACCGTGTG 300

QY 374 GAGAGAGGCGCGCTGTGACCGCGCGGAGAAAGTGGGCTTCCAGCGCGGCTAAG 433

DB 301 GAGAGAGGCGCGCTGTGACCGCGCGGAGAAAGTGGGCTTCCAGCGCGGCTAAG 360

QY 434 GAGAGAGGCGCGAGCTGTGCGCGGAGACTGCGAGCGCTGTGTGCTGTAGCTCGCGG 493

DB 361 GAGAGAGGCGCGAGCTGTGCGCGGAGACTGCGAGCGCTGTGTGCTGTAGCTCGCGG 420

QY 494 CTGATGCGGCGAGCAACCGCGCTGTGAGCTGACGCGCGCTGCGATGCTTTTGTAC 553

DB 421 CTGATGCGGCGAGCAACCGCGCTGTGAGCTGACGCGCGCTGCGATGCTTTTGTAC 480

QY 554 TTCTTCAGAGACCCCTTCCACCTGCTTTTGGAGAAACAGCTGTGCTCCAGGCTTTCTG 613

DB 481 TTCTTCAGAGACCCCTTCCACCTGCTTTTGGAGAAACAGCTGTGCTCCAGGCTTTCTG 540

QY 614 TCATGCTGTTTAAACAAGCTTCACTTATCTGTGACACAGATTAATATGATTTTAA 673

DB 541 TCATGCTGTTTAAACAAGCTTCACTTATCTGTGACACAGATTAATATGATTTTAA 600

QY 674 CTTTAAACCGCTTCTACCTGCGCACTGTGACCACTAAATGACAGATGTGTGAGAA 733

DB 601 CTTTAAACCGCTTCTACCTGCGCACTGTGACCACTAAATGACAGATGTGTGAGAA 660

QY 734 AGAAGTGAAGGAAAGCACTTCCCGCAACCGCAAGCTTTTATCTGTAATGATCAAGGA 793

DB 661 AGAAGTGAAGGAAAGCACTTCCCGCAACCGCAAGCTTTTATCTGTAATGATCAAGGA 720

QY 794 GTCTGAGTGTGTATTTGCGCAGTGTATTAACTTGTGACAAGTACTGAGTGTGAGAC 853

DB 721 GTCTGAGTGTGTATTTGCGCAGTGTATTAACTTGTGACAAGTACTGAGTGTGAGAC 780

QY 854 AAGAATGCAATGCGCTTCTCTTGAAGTGAAGAA 887

DB 781 AAGAATGCAATGCGCTTCTCTTGAAGTGAAGAA 814

# RESULT 3

ID AA290039 standard; cDNA; 582 BP.

XX AA290039;

DT 09-MAY-2000 (first entry)

DE Hydrophobic domain containing protein clone HP02403 coding sequence.

XX Hydrophobic domain; clone HP02403; nutritional supplement; SCID; HIV;

KW cell proliferation; immune stimulant; immune deficiency; tumour; pain;

KW rheumatoid arthritis; insulin dependent diabetes mellitus; fertility;

KW myasthenia gravis; haematopoiesis regulator; tissue growth; depression;

XX anti-inflammatory; infection; bodily characteristic; ss.

OS Homo sapiens.

PN WO200000506-A2.

XX 06-JAN-2000.

XX 18-JUN-1999; 99WO-JP003242.

XX 26-JUN-1998; 98JP-00180008.

PA (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

PI Kato S, Kimura T;

XX WPI: 2000-160665/14.

DR P-PSDB: AAY78802.

PT Novel human proteins having hydrophobic domains used for research and

XX diagnostic purposes.

PS Claim 3; Page 84; 117pp; English.

CC This sequence represents the hydrophobic domain containing protein, clone

CC HP061 coding region. The sequence is isolated from a human stomach

CC cancer cell line. The HP02403 protein contains one putative transmembrane

CC domain. The protein shows homology to the Japanese quail apoptosis

CC regulator NR-13. The invention relates to human proteins with hydrophobic

CC domains, the DNA and the cDNA encoding them. The polynucleotides and

CC proteins are predicted to have biological activities which make them

CC suitable for treating, preventing or ameliorating medical conditions in

CC humans and animals. Suggested activities include nutritional activity

CC (nutritional source or supplement); cytokine and cell

CC proliferation/differentiation activity; immune stimulating (e.g. as

CC vaccines) or suppressing activity (e.g. to treat various immune

CC deficiencies such as SCIDS or HIV, connective tissue disease, systemic

CC lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary

CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin

CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease

CC and autoimmune inflammatory eye disease, as well as asthma, allergies and

CC organ transplantation; haematopoiesis regulating activity (e.g. in

CC treatment of myeloid or lymphoid cell deficiencies); tissue growth

CC activity (e.g. wound healing and tissue repair, ulcers, burns,

CC periodontal disease); activin/inhibin activity; chemotactic/chemokinetic

CC activity; haemostatic and thrombolytic activity (e.g. treating

CC haemophilias); receptor/ligand activity; anti-inflammatory activity; and

CC tumour inhibition activity. The polynucleotides are also stated to be

CC useful for gene therapy. Other activities include inhibiting infections

CC caused by bacteria, fungi, viruses and other parasites (e.g. Hepatitis,

CC malaria); effecting bodily characteristics such as, e.g. weight, colour,

CC skin, effecting biorhythms or cardiac cycles; enhancing fertility;

CC treatment of depression; treatment of pain; hormonal or endocrine

CC activity. The polynucleotides may also be used for recombinant expression

CC of the protein

SO Sequence 582 BP; 85 A; 193 C; 191 G; 113 T; 0 U; 0 Other;

Query Match	65.6%	Score 582;	DB 3;	Length 582;
Best Local Similarity	100.0%;	Pred. No. 4e-121;		
Matches 582;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	80	ATGGCCGACCCGCTCGGGAGGCGACCCGAGCTGTTCCTGAGCGACATACCTGGGGTACTGC	139
Db	1	ATGGCCGACCCGCTCGGGAGGCGACCCGAGCTGTTCCTGAGCGACATACCTGGGGTACTGC	60
QY	140	GCCCCGGAAACCCGGGACCCCGAGCCGGGCGCATCCAGCCCCGAGGCGCGCTGTGGC	199
Db	61	GCCCCGGAAACCCGGGACCCCGAGCCGGGCGCATCCAGCCCCGAGGCGCGCTGTGGC	120
QY	200	TCCGGGGCCGCCAGGTAAAGGCAGATTACCGGTCTTTTCTCCGCTTACCTCGGCTAC	259
Db	121	TCCGGGGCCGCCAGGTAAAGGCAGATTACCGGTCTTTTCTCCGCTTACCTCGGCTAC	180
QY	260	CCCCGGAAACCGCTTGAGCTGGTGGGCGCATAGGCGGATTCCGTTGCTCCGACAGCCCC	319
Db	181	CCCCGGAAACCGCTTGAGCTGGTGGGCGCATAGGCGGATTCCGTTGCTCCGACAGCCCC	240
QY	320	GAGCCCACTGGGGGACAGATGGTGAACGCTCGTACCTTCGACAGGAGACGCTGCTGAGAGA	379
Db	241	GAGCCCACTGGGGGACAGATGGTGAACGCTCGTACCTTCGACAGGAGACGCTGCTGAGAGA	300
QY	380	GAGCCGCTGTGTGACCGCCCTGTGTGAAGAAAGTGGGGCTTCCAGCCGCGCTAAAGAGACAG	439
Db	301	GAGCCGCTGTGTGACCGCCCTGTGTGAAGAAAGTGGGGCTTCCAGCCGCGCTAAAGAGACAG	360
QY	440	GAGGGCGACGTGGCCCGGAGCTGCCAGGCGCTGGTGGCCCTGTGTGAGCTCGGGCTCATG	499
Db	361	GAGGGCGACGTGGCCCGGAGCTGCCAGGCGCTGGTGGCCCTGTGTGAGCTCGGGCTCATG	420
QY	500	GGGCAGCACCGCGCCTGTGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTGTGTCACTTCTTC	559
Db	421	GGGCAAGCACCGCGCCTGTGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTGTGTCACTTCTTC	480
QY	560	AGGACCCCTTTTTCACCTGGCTTTTGTGAGAAAACAGCTGGTCCAGGCTTTTCTGTCAATGC	619
Db	481	AGGACCCCTTTTTCACCTGGCTTTTGTGAGAAAACAGCTGGTCCAGGCTTTTCTGTCAATGC	540
QY	620	TTGTTAACAACAGCCCTCACTTATCTCTGACACGATTAATA	661
Db	541	TTGTTAACAACAGCCCTCACTTATCTCTGACACGATTAATA	582

RESULT 4  
AAH47022  
ID AAH47022 standard; cDNA; 522 BP

PN	WO200157060-A1.
XX	
PD	09-AUG-2001.
XX	
PF	31-JAN-2001; 2001WO-US003080

XX 01-FEB-2000; 2000US-0179487P.  
PR 07-FEB-2000; 2000US-0180697P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
FA  
XX  
XX  
PI Ruben SM, Duan DR, Ni J;  
XX  
XX WPI: 2001-476279/51.  
DR P-PSDB; AAB85666.  
XX  
XX Nucleic acids encoding human Bcl-2-like polypeptides, useful for  
PT preventing, diagnosing and/or treating.  
XX  
XX Claim 1; Page 276; 285dp; English.  
XX

CC The invention provides nucleic acid molecules (NAM1) encoding a human Bcl-  
CC 2-1-like polypeptides (PEP1). The NAM1 and PEP1 may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate Bcl-2-like polypeptides' expression. The NAM1 may be used  
CC to produce the soluble Bcl-2-like polypeptides by standard recombinant  
CC methodology. The polypeptides may also be used as antigens in the  
CC production of antibodies against Bcl-2 and in assays to identify  
CC modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies  
CC and antagonists may be used to down regulate expression and activity. The  
CC anti-PEP1 antibodies may also be used as diagnostic agents for detecting  
CC the presence of Bcl-2 polyps in samples (e.g. by enzyme linked  
CC immunosorbent assay (ELISA)). Disorders that may be prevented, diagnosed  
CC and/or treated by the above methods include, immunodeficiencies (e.g. a  
CC gammaglobulinemia and B cell lymphoproliferative disorder), autoimmune  
CC disorders (e.g. rheumatoid arthritis and Grave's disease), allergic  
CC reactions, inflammations, respiratory diseases and cardiovascular  
CC disorders (a full list of disorders is given in the specification). The  
CC present sequence represents a human Bcl-2-like polypeptide encoding cDNA  
CC  
CC  
CC Sequence 522 BP; 102 A; 148 C; 154 G; 118 T; 0 U; 0 Other;  
XX

Query Match	57.1%;	Score 506.8;	DB 4;	Length 522;
Best Local Similarity	99.4%;	Pred. No. 3.2e-104;		
Matches 519; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1

QY	270	GCTTGAGCTGGTGGCGCTGATGGGGGATTCGTGCTTCGACAGCCCCGCGCCACCT	329
Db	1	GCTTGAGCTGGTGGCGCTGATGGGGGATTCGTGCTTCGACAGCCCCGCGCCACCT	60
QY	330	GGGGCAGAGTGGTGAAGCTCTGTGACTTCGACAGGACGCTGTGAGAGAGGGCGCTGG	389
Db	61	GGGGCAGAGTGGTGAAGCTCTGTGACTTCGACAGGACGCTGTGAGAGAGGGCGCTGG	120
QY	390	TGACCGGCGCGTGGGAAAGATGGGGGCTTCACCGCGGCTTAAGAGAGAGAGGGAGAG	449
Db	121	TGACCGGCGCGTGGGAAAGATGGGGCTTCACCGCGGCTTAAGAGAGAGAGGGAGAG	180
QY	450	TGCGCCCGGAGCTGCCAGCGGCGCTGTGTGGCCTTGTGAGCTCGCGGCTCATGGGGCAGACCC	509
Db	181	TGCGCCCGGAGCTGCCAGCGGCGCTGTGTGGCCTTGTGAGCTCGCGGCTCATGGGGCAGACCC	240
QY	510	GCGCGTGGTGCAGAGCTCAGGGCGGCTGGGATGGCGCTTTGTCACTTTCACGACCCCGCT	569
Db	241	GCGCGTGGTGCAGAGCTCAGGGCGGCTGGGATGGCGCTTTGTCACTTTCACGACCCCGCT	300
QY	570	TTTCCACTGGCTTTTGGAGAAACAGCTGGTCAAGGCTTTTGTGTCATGCTTGTAAACA	629
Db	301	TTTCCACTGGCTTTTGGAGAAACAGCTGGTCAAGGCTTTTGTGTCATGCTTGTAAACA	360
QY	630	CAGCCTTCAATTATCTCTGGACAGATTATATGATTTTAAACCTTTTAAACCCGCTTCT	689
Db	361	CAGCCTTCAATTATCTCTGGACAGATTATATGATTTTAAACCTTTTAAACCCGCTTCT	420
QY	690	ACCTGCGCAACTGTGACCACTTAATGACAGATGTGTGAGACAAACATCGAGGGGAAAGC	749
Db	421	ACCTGCGCAACTGTGACCACTTAATGACAGATGTGTGAGACAAACATCGAGGGGAAAGC	480

Qy 750 ACCTTCCCCACCCGAGCG-TTTTATCTGATGATCAACA 790  
Db 481 ACCTTCCCTCACCCGAGCGTTTCTTACTGATGATCAACA 522

## RESULT 5

ABK41913

ID ABK41913 standard; cDNA; 548 BP.

AC ABK41913;

XX 21-MAY-2002 (first entry)

DE cDNA encoding novel human connective tissue related polypeptide #301.

XX Human; connective tissue related disorder; cancer; gene therapy;  
KM cytosolic; gene; ss.

XX Homo sapiens.

OS WO00155343-A1.

XX 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001322.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

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PR 14-AUG-2000; 2000US-0224519P.

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PR 23-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

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PR 01-SEP-2000; 2000US-0229345P.

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PR 05-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 06-SEP-2000; 2000US-0231242P.

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PR 12-SEP-2000; 2000US-0231968P.

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PR 14-SEP-2000; 2000US-0232398P.

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PR 21-SEP-2000; 2000US-0234223P.

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PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX MPI; 2001-565190/63.
XX
XX P-PSDB; AAU86735.
XX
XX Nucleic acid encoding novel connective tissue associated polypeptides,
XX PT used in diagnosing, preventing, treating or ameliorating a disorder such
XX as cancer or rheumatoid arthritis.
XX
XX Claim 4; SEQ ID NO 311; 673bp; English.
XX
XX The present invention relates to the isolation of novel human connective
XX tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
XX (cDNA and genomic) sequences encoding them. The sequences of the
XX invention are useful in the diagnosis, treatment, prevention and/or
XX prognosis of diseases associated with connective tissue(s), including
XX cancer. The polynucleotide sequences of the invention are also useful in
XX gene therapy. ABK41613-ABK42101 represent cDNA sequences encoding the
XX novel human connective tissue related polypeptides. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pcr_sequences
XX
XX Sequence 548 BP; 99 A; 154 C; 167 G; 121 T; 0 U; 7 Other;
XX
XX Query Match 51.5%; Score 457.2; DB 4; Length 548;
XX Best Local Similarity 98.2%; Pred. No. 4,6e-93;
XX Matches 481; Conservative 2; Mismatches 5; Indels 2; Gaps 2;
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DB 359 CAGGACCCCTTTCACCTGGCTTTTGTGAGAAAACAGCTGTGCTCAGGCTTTCGTCTCAG 418
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DB 539 TGAGGGAAG 548
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XX
XX RESULT 6
XX ADB59580
XX ID ADB59580 standard; cDNA; 548 BP.
XX
XX ADB59580;
XX
XX 04-DEC-2003 (first entry)
XX
XX DE Connective tissue related polynucleotide #301.
XX
XX cyrostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;
XX antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;
XX antidiabetic; antiallergic; antiaesthetic; dermatological;
XX nephrotoxic; virucide; fungicide; antibacterial; antiparasitic;
XX gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
XX systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;
XX cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disease;
XX atherosclerosis; myocarditis; cardiopulmonary bypass complication;
XX autoimmune disease; multiple sclerosis; allergic reaction; asthma;
XX rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
XX gastrointestinal disorder; inflammatory bowel disease;
XX organ transplant rejection; immune system disorder; Brucella disease;
XX X-linked lymphoproliferative syndrome;
XX B-cell lymphoproliferative disorder; HIV; AIDS; infection;
XX chromosome identification; chromosome mapping;
XX connective tissue related polynucleotide; gene; ss.
XX
XX Homo sapiens.
XX
XX FN US2003054375-A1.
XX
XX PD 20-MAR-2003.
XX
XX PF 07-MAR-2002; 2002US-00092154.
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XX 31-JAN-2000; 2000US-0179065P.
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XX					
PA	(HUMA-1) HUMAN GENOME SCI INC.				
PI	Rosen CA, Ruben SM, Barash SC;				
XX					
DR	WPI: 2003-634869/60.				
DR	P-PSDB; ADB60069.				
XX					
PT	New connective tissue-related polypeptides and polynucleotides, useful				
PT	for treating, preventing and/or prognosing e.g. disorders of connective				
PT	tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or				
PT	neoplasias.				
XX					
PS	Claim 1; SEQ ID NO 311; 240bp; English.				
XX					
CC	The invention describes an isolated nucleic acid molecule (I), which				
CC	comprises a sequence that is at least 95 % identical to a connective				
CC	tissue-related polynucleotide encoding connective tissue antigens (CTA).				
CC	The polypeptide or polynucleotide is useful for preventing, treating, or				
CC	ameliorating medical conditions in a mammal. The connective tissue				
CC	polypeptides, polynucleotides and antibodies are particularly useful for				
CC	treating, preventing and/or prognosing disorders of connective tissues				
CC	(e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,				
CC	scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or				
CC	neoplasias (e.g. leukemia), neurodegenerative disorders (e.g.				
CC	Alzheimer's disease, or Parkinson's disease), cardiovascular diseases				
CC	(e.g. atherosclerosis, myocarditis or cardiopulmonary bypass				
CC	complications), autoimmune diseases (e.g. systemic lupus erythematosus,				
CC	rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.				

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DB 61 CCAGCGCTCCGCTTGAAGTGGGCGCTGATGCGGATTCGCTCTCCGACAGCCC 120
QY 319 CCGCCCCCTTGGGGGAGAGTGTGACCTGCTGACCTTCCGAGGAGAGCTGCTGGAAG 378
    |||
DB 121 CCGCCCCCTTGGGGGAGAGTGTGACCTGCTGACCTTCCGAGGAGAGCTGCTGGAAG 179
QY 379 AGGCGCGCTGAGACCGCCCGGTGGAAGAGTGGGGCTTCCAGCGCGCTTAAAGAGCA 438
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RESULT 7
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XX
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XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 30995.
XX
KW Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PE 01-SEP-2001; 2001MO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
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PS Claim 12; 56bp + Sequence Listing; 56bp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CPG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNPs); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABO3410-
CC ABO54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 874 BP; 144 A; 90 C; 320 G; 320 T; 0 U; 0 Other;
XX
Query Match 36.6%; Score 324.6; DB 6; Length 874;
Best Local Similarity 75.1%; Pred. No. 3.3e-63;
Matches 405; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
QY 1 CCGGCGAAGAAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 100 CCGGCTTAAAGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159
QY 61 GTTGGGAGAGCGCACACCATGAGCGAGCCGCTGCGGAGAGCGAGAGAGAGAGAGAGAGAGAG 120
DB 160 GTTGGGAGAGCGCATTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 219
QY 121 CGACTACTGAGGAGTACTGCGCCCGGAGAACCGGAGAACCGGAGAGAGAGAGAGAGAGAGAG 180
DB 220 CGATTATTGGGAGATGATGCTGCGGAGATGCGGAGATGCGGAGATGCGGAGATGCGGAGAT 279
QY 181 CGAGGCGCGCGCTGCTGCGCTGCGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 280 CGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 339
QY 241 CTCGCGCTACCTGCGCTACCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 340 TTTGCTTATTTCGCTTATTTCGCTTATTTCGCTTATTTCGCTTATTTCGCTTATTTCGCTT 399
QY 301 CGTGTCTCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 400 CGTGTCTCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
QY 361 AGGAGCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 460 AGGAGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
QY 421 GCGGCGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 520 GTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 579
QY 481 GCTGAGCTGCGGCTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
DB 580 GTTGAAGTTCGCGGTTTATGAGGAGTATGAGGAGTATGAGGAGTATGAGGAGTATGAGGAG 638

RESULT 8
ABO44405/C
ID ABO44405 standard; DNA; 874 BP.
XX
AC ABO44405;
XX
DT 12-JUL-2002 (first entry)
```

XX XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 30996.  
 DE  
 XX  
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200218632-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PF 01-SEP-2001; 2001WO-EP010074.  
 XX  
 PR 01-SEP-2000; 2000DE-01043826.  
 PR 05-SEP-2000; 2000DE-01044543.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
 XX  
 DR WPI; 2002-371829/40.  
 XX  
 PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons  
 PT from chemically treated DNA.  
 XX  
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
 XX  
 CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNP's); and (11) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation  
 CC status of many C residues to be determined simultaneously. ABQ13410-  
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention  
 CC  
 XX  
 SQ Sequence 874 BP; 320 A; 320 C; 90 G; 144 T; 0 U; 0 Other;  
 Query Match 36.6%; Score 324.6; DB 6; Length 874;  
 Best Local Similarity 75.1%; Pred. No. 3,3e-63;  
 Matches 405; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 241 CTCGCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGGCGCTGATGCGGATTTC 300  
 DB 535 TTTCGTTATTTTCGTTATTTTCGGAATTCGTTGAGTTGGTGGTTGATGCGGATTTC 476  
 QY 301 CGTGCTTCGACAGACCCCGGCCCCACCTGCGGAGAGTGTGACGCTCGACCTTCGC 360  
 DB 475 CGTGTTCGATAGTTTCGTTTATTTTGGGGGTGAGTGTGACGTTTCGATTTTCGT 416  
 QY 361 AGGACGCTGCTGAGAGAGAGGCGCTGTGACCCCGGTGTGAAGATGGGCGTTTCCA 420  
 DB 415 AGGACGTTGTGAGAGAGAGGCGTGTGTATGTTTCGTTGAAGAGTGGGTTTTC 356  
 QY 421 GCCGCGCTAAAGAGAGAGGCGACGTCGCCCGGAGCTGCCAGCGCTGTGGCCTT 480  
 DB 355 GTCCGCGTTAAAGAGTGAAGGCGGACGTCGTTCCGATTTGTTAGCCTTTGGTGGTTT 296  
 QY 481 GCTGAGCTCGCGCTCATGCGGCGACGACCGGCTGCTGACGCTCAGGCGGCTGGG 539  
 DB 295 GTTGAATTGCGGCTTATGCGGTTAGTATCGGTTTGGTTTGAAGGCGGTTTGGG 237

RESULT 9  
 ABQ44403  
 ID ABQ44403 standard; DNA; 874 BP.  
 XX  
 AC ABQ44403;  
 XX  
 DT 12-JUN-2002 (first entry)  
 XX  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 30994.  
 XX  
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200218632-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PF 01-SEP-2001; 2001WO-EP010074.  
 XX  
 PR 01-SEP-2000; 2000DE-01043826.  
 PR 05-SEP-2000; 2000DE-01044543.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
 XX  
 DR WPI; 2002-371829/40.  
 XX  
 PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons  
 PT from chemically treated DNA.  
 XX  
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
 XX  
 CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,





XX WO2003020220-A2.  
 PN 13-MAR-2003.  
 PD 30-AUG-2002; 2002WO-US027886.  
 PF 30-AUG-2001; 2001US-0316323P.  
 PR 31-AUG-2001; 2001CA-02356540.  
 XX (UYEM-) UNIV EMORY.  
 PA Wallace DC, Levy S, Kerstam K, Procaccio V;  
 PI WPI; 2003-300821/29.  
 DR WPI; 2003-300821/29.  
 PT Array containing probes for genes involved in mitochondrial biology,  
 PT useful for determining mitochondrial biology gene expression profiles for  
 PT use in diagnosing pathologies and identifying biochemical pathways.  
 PS Claim 2; SEQ ID NO 2360; 201pp; English.

CC The invention relates to a novel array comprising at least two isolated  
 CC nucleotide molecules, each molecule having a sequence capable of uniquely  
 CC hybridising to a nucleic acid molecule which is an expression product of  
 CC a gene involved in mitochondrial biology. The array comprises two or more  
 CC isolated nucleic acid molecules or spots, each molecule having a sequence  
 CC chosen from sequence of 994 human probes and 2046 mouse probes. An array  
 CC of the invention is useful for determining an expression profile of a  
 CC mouse or human sample containing nucleic acid, by contacting the array  
 CC with the sample under conditions allowing selective hybridisation, and  
 CC measuring hybridisation of nucleic acid in the sample to the array to  
 CC produce an expression profile. The array is also useful for determining  
 CC an expression profile of a first labelled sample containing nucleic acid  
 CC relative to a second, differently labelled sample containing nucleic  
 CC acid. The second sample is a reference or a standard. An array is useful  
 CC for determining an expression profile diagnostic of an energy-metabolism-  
 CC related physiological condition. An array of the invention is useful for  
 CC determining mitochondrial biology gene expression profiles of organisms,  
 CC such as human, mice and closely related species, tissue and organs of  
 CC such organisms, which are useful for determining expression profiles  
 CC diagnostic of energy metabolism-related physiological conditions,  
 CC diagnosing such physiological conditions, identifying biochemical  
 CC pathways, genes, and mutations involved in such physiological conditions,  
 CC identifying therapeutic agents useful for preventing and/or treating such  
 CC physiological conditions, evaluating and/or monitoring the efficacy of  
 CC such therapies, and creating and identifying animal models of human  
 CC energy metabolism-related physiological conditions. An array is also  
 CC useful for defining expression signatures or profiles for mitochondrial  
 CC diseases, as well as distinguishing clinical disorders that result from  
 CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,  
 CC apoptosis and aging. An array of the invention contains probes of genes  
 CC not previously recognised to participate in mitochondrial biology. The  
 CC sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA  
 CC clones used to make the probes of the invention. Some sequences are not  
 CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,  
 CC 1906, 2408 and 2643.  
 XX

XX Sequence 835 BP; 238 A; 200 C; 185 G; 212 T; 0 U; 0 Other;

Query Match 17.4%; Score 154; DB 10; Length 835;  
 Best Local Similarity 62.7%; Pred. No. 7; 7e-25;  
 Matches 291; Conservative 0; Mismatches 165; Indels 8; Gaps 3;

QY 378 GAGGGCCGCTGTGACCCCGGTGAAGAAGTGGGCTTCCAGCCGCGCTTAAGAGAC 437  
 DB 816 GCGGACACTTATGATCAAGGCCCTTACATGCTGTCAAGAGAAAGGAGATCTGGGGA 757  
 QY 438 AGGAGGGGAGCTCGCCGCGGAGCTGCAGCGGCTGTGCTGAGCTCGGGGCTCA 497  
 DB 756 ATCGTGTATTAAGACCCGAGACTGTGTCTTATATGTAACCTTCTGTAATATGCTCA 697  
 QY 498 TGGGG---CAGCACCGCGCTGTGCAAGGCTCAAGGGCGGCTGGAGATGGCTTTTGTCACT 554

DB 696 TGGGCGCTGCGCACCGGCCAGCTGAGGCTCTCGGGGCTGGGATGGCTTTGCGCGCT 637  
 QY 555 TCTTCAGAACCCCTTTCACATGCTTTTGGAGAAAAACACTGCTCCAGGCTTTTCGT 614  
 DB 636 TCTTCAGAAATCTTTCACGCTCTGAGAAAGTTCTGATTAAGGCTTTTCGT 577  
 QY 615 CATGCTTGTAAACAAGCCTTTCATTTATCTGGAACAGATTATATGATTTTAAAC 674  
 DB 576 CAGGCTTCTTTCAGAACCCATCTTTTATCTGGAACGTTTAT---AAGTTTAAAT 521  
 QY 675 TTTTAACCCGCTTCTACCTGCGCAACTGTGA CCACTAATATGACAGATGTGTGAGAACAA 734  
 DB 520 TTTTAAGCGATCTTACCTACTACCTGTGAACCTCTAAGAGAACATTCGGTAATG 461  
 QY 735 GAATGAGAGAAAGACCTTCCCAACCCAGAGAGTTTATGTAATGATTAAGAGAG 794  
 DB 460 GATTAAGAACTGAGAAAGTCTTCAGCCTAAGAGACATTTCTACCTGCAATGC-TACATGAG 402  
 QY 795 TCTGAGGTGTGATTTTGGCCAGTGTTTTAACTGTGACAAGTA 838  
 DB 401 TCTGAGTGTGATTTGAGGCGGCGAGCATTTGAAGAGGCGCCATGTA 358

RESULT 13  
 ADD34583  
 ID ADD34583 standard; DNA; 338 BP.

AC ADD34583;

DT 15-JAN-2004 (first entry)

DE Mouse mitochondrial DNA sequence SEQ ID NO:2361.

KM ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;  
 KM mitochondrial disease; oxidative phosphorylation dysfunction;  
 KM oxidative stress; apoptosis; aging.

OS Mus musculus.

PN WO2003020220-A2.

PD 13-MAR-2003.

PF 30-AUG-2002; 2002WO-US027886.

PR 30-AUG-2001; 2001US-0316323P.

PR 31-AUG-2001; 2001CA-02356540.

PA (UYEM-) UNIV EMORY.

PI Wallace DC, Levy S, Kerstam K, Procaccio V;

DR WPI; 2003-300821/29.

PT Array containing probes for genes involved in mitochondrial biology,  
 PT useful for determining mitochondrial biology gene expression profiles for  
 PT use in diagnosing pathologies and identifying biochemical pathways.

PS Claim 2; SEQ ID NO 2361; 201pp; English.

XX The invention relates to a novel array comprising at least two isolated  
 XX nucleotide molecules, each molecule having a sequence capable of uniquely  
 XX hybridising to a nucleic acid molecule which is an expression product of  
 XX a gene involved in mitochondrial biology. The array comprises two or more  
 XX isolated nucleic acid molecules or spots, each molecule having a sequence  
 XX chosen from sequence of 994 human probes and 2046 mouse probes. An array  
 XX of the invention is useful for determining an expression profile of a  
 XX mouse or human sample containing nucleic acid, by contacting the array  
 XX with the sample under conditions allowing selective hybridisation, and  
 XX measuring hybridisation of nucleic acid in the sample to the array to  
 XX produce an expression profile. The array is also useful for determining  
 XX an expression profile of a first labelled sample containing nucleic acid

relative to a second, differently labelled sample containing nucleic acid. The second sample is a reference or a standard. An array is useful for determining an expression profile diagnostic of an energy-metabolism-related physiological condition. An array of the invention is useful for determining mitochondrial biology gene expression profiles of organisms, such as human, mice and closely related species, tissue and organs of such organisms, which are useful for determining expression profiles diagnostic of energy metabolism-related physiological conditions, diagnosing such physiological conditions, identifying biochemical pathways, genes, and mutations involved in such physiological conditions, identifying therapeutic agents useful for preventing and/or treating such physiological conditions, evaluating and/or monitoring the efficacy of such therapies, and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The sequences shown in ADBD31224-ADBD35260 represent murine mitochondrial DNA clones used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905, 1906, 2408 and 2643.

PI	Karagiri F, Quan S, Tao Y, Whitcham S, Xie Z, Zhu T, Zou G;
XX	
DR	WP1: 2003-175290/17.
XX	
PT	Identifying at least one gene involved in plant resistance or response to
PT	pathogenic infection for conferring resistance or tolerance to a plant to
PT	bacterial, fungal or viral infection by determining or detecting plant
PT	gene expression.
XX	
PS	Claim 27; SEQ ID NO 5263; 899pp; English.
XX	
CC	The present invention relates to a method (M1) for identifying genes
CC	involved in plant resistance or response to pathogenic infection. M1
CC	comprises identifying a gene whose expression is significantly altered in
CC	the incompatible interaction of plant gene expression relative to
CC	expression of the gene in an uninfected plant, in a mutant plant that
CC	does not express a gene associated with response to pathogenic infection,
CC	or in a corresponding incompatible or compatible interaction. (M1) is
CC	useful for conferring resistance to resistance or tolerance to a plant to
CC	bacterial, fungal or viral infection. The present sequence was used to
CC	illustrate the invention.
XX	
SQ	Sequence 2000 BP, 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 7.7%; Score 68; DB 8; length 2000;

Query Match	10.0%	Score 88.6;	DB 10;	Length 338;
Best Local Similarity	64.3%;	Pred. No. 3.2e-10;		
Matches 133; Conservative	0;	Mismatches 74;	Indels 0;	Gaps 0

Seq	Conservative	Idels	Gaps
7 AGAAAAACGAGGCCCCCCCCAGACAGAGGCCGACCATGGTTGACCAATTGCG	66	12	3
86; Mismatches 322;			

QY	86	AACCCGCTGACGGAGACGACACCGAGCGTGTGCTGAGCGACTACCTGGGGGATACGTGGCCGG	145
Db	132	GACCCACTGACATGAACGCACTAGACGGCTGCTGTCTGACTTACATATTTCTTTCGGACCG	191
QY	146	GAACCCGGACACCCCGAGCCGGCGGCATTCACGCCGAGGCGCGCGTGTGCGCTCCGG	205
Db	192	GAGCCGAGACACCCGAGAGCCACCGGCCAAGTCTGTGTGAGGCGGGCTTGTCTTGGCTCTGTG	251
QY	206	GCCGCGCAGGTTACGGCAGATTACCGGTCCTTTTCTCGGCTTACCTGTGGCTAACCCCGGG	265
Db	252	ACTAGGAGAGATTCACGACGAGAGACCAAGATTTTTTTTCTCTTCTGTGCAAGACGGGGG	311
QY	266	AACCGCTTCGAGCTGTGTGGCGCTGATG	292
Db	312	AATGCGCTGTGAGCTGTGTGAACAGATG	338

[illegible]

```

RESULT 14
ADA71938
ID ADA71938 standard; DNA; 2000 BP.
XX
XX
AC ADA71938;
XX
XX
20-NOV-2003 (first entry)
DT
XX
XX
DE Rice gene, SEQ ID 5263.
XX
XX
Plant; bacterial infection; fungal infection; viral infection; rice
XX
XX
gen; db.
XX
XX
Oryza sativa.
OS
XX
PN MO2003000898-A1.
XX
XX
03-JAN-2003.
XX
XX
22-JUN-2001; 2001MO-IB001105.
XX
XX
22-JUN-2001; 2001MO-IB001105.
XX
XX
PR
XX
XX
(SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX
Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

```

307 CTCGACAGACCCCGGCCCTTGGGGCAGAGTGTGACGCTCGTGAACCTTCGACAGGAC 366  
320 SRMAMMYKMYWYGYKGMKRGWAGBMMMSMCWMSJACYYMRBMRMTLRBRWAKKS 379  
367 GCTGTGGAGAGAGGCCGCTGTGATCCGCCCGGAGGAAGAAGTGGGGCTTCAGCCGGC 426  
380 SRTBRKKKKKCMKKKKTKKRRGTSSRMSCRARMMKCRSRAMKMGRCGMYCKMKRY 439  
427 GCTAAGACGACGAGGGCGACGTCGCCCGGACCTGCACGCGCTGTGGCCCTTGCTGAG 486  
440 GMMWKSJMKRMSKVKWMSRYMYRWRKCKCSRTYMMGTRGGMMGTGRCCRYKRSGBMKK 499  
487 CTGCGCGCTCATGGGGCAGCACCGCGCTGTGCTGC - AGGCTCAGGGCGGCTGGGATGGC 544  
500 CRRRRGMYWRRMRJYMSARJYMRJYCARKKYSTSARKARCMYRGGKYTYAGMMMKRY 559  
545 TTTTGTCACCTTCCTCAGAGCCCTTCCTTCACGTGCTTTTGGAGAAAACGCTGTCCAG 604  
560 KBMYWYKMMWYKRYKSKSMYCKMSYVASCMKSRKAGAKMKCRKSMSAMSKMSRSRK 619  
605 ----GCTTTCTGTCAGCTTGTTTAACACAGCTTCAATTATCTCTGACACACTATT 660  
620 CRKCAKRSKSAKRYAMMGAMTSGSRMSRWKSYTCWRWGSNKSCCTTMYMYSKTYAKY 679  
661 ATGAGTTTAAACCTTTTAAACCCGCTTCTACCTGCCCAACTGTGACCACTAAAGACAG 720

```
Db      680 GSYMYRYRAMCMYMMWYRYRSMYTMAMYTSTTMAATGMKXSGRYTSMYKCKC 739
QY      721 ATGTGTGAACAACAACGACGAGCAACCTTCCACCCGACACTTTTATCGA 780
Db      740 SKKYSSMYMWMMAKTRMRRYATRMWMMWYRSMKMYTCMGMWYMYMTYMKM 799
QY      781 AT 782
Db      800 RY 801
```

## RESULT 15

```
ABN42801
ID      ABN42801 standard; DNA; 60 BP.
```

```
AC      ABN42801;
```

```
DT      15-JUL-2002 (first entry)
```

```
DE      Human spliced transcript detection oligonucleotide SEQ ID NO:15549.
```

```
KW      Human; mouse; rat; splice transcript; detection; RNA transcript;
```

```
KW      splice variant; transcriptome; oligonucleotide library; ss.
```

```
OS      Homo sapiens.
```

```
PN      MO200210449-A2.
```

```
PD      07-FEB-2002.
```

```
PF      20-JUL-2001; 2001WO-IB001903.
```

```
PR      28-JUL-2000; 2000US-0221607P.
```

```
BR      02-MAY-2001; 2001US-0287724P.
```

```
PA      (COMP-) COMPUGEN INC.
```

```
PI      Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
```

```
DR      WPI; 2002-257383/30.
```

```
PT      New oligonucleotide libraries comprising oligonucleotides which
PT      selectively hybridize to mRNAs transcribed from a transcription unit of a
PT      genome, useful for detecting tissue-, pathology-, and developmental-
PT      specific genes.
```

```
PS      Example 1; SEQ ID NO 15549; 47bp; English.
```

```
XX      The present invention describes oligonucleotide libraries for detecting
CC      messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC      )transcriptome comprises messenger RNAs transcribed from multiple
CC      transcription units that populate a genome. The library comprises several
CC      oligonucleotides, each capable of hybridizing selectively to a set of
CC      messenger RNAs transcribed from a given transcription unit of the genome,
CC      which encodes one or more messenger RNA splice variants. The
CC      oligonucleotide libraries are useful for detecting mRNAs from a
CC      biological sample, in expression profiling studies, in qualitatively or
CC      quantitatively characterizing the corresponding transcriptome, and in
CC      detecting RNA transcripts and splice variants of human or animal
CC      transcriptomes. The libraries may also be used as specialised mini
CC      libraries to detect transcripts of a sub-transcriptome under a particular
CC      biological or pathological state, and so allowing the detection of tissue
CC      - and pathology-specific genes such as those genes only expressed in
CC      specific tissue under a specific pathological condition; to detect
CC      developmental specific genes; and to detect RNA transcripts and splice
CC      variants of a transcriptome of a patient suffering from a particular
CC      disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC      rats, humans and mice, which are used in the exemplification of the
CC      present invention. N.B. The sequence data for this patent did not form
CC      part of the printed specification, but was obtained in electronic format
CC      directly from WIPO at fcp.wipo.int/pub/published_pct_sequences
```

SQL Sequence 60 BP; 9 A; 16 C; 13 G; 22 T; 0 U; 0 Other;

Query Match 6.8%; Score 60; DB 6; Length 60;

Best Local Similarity 100.0%; Pred. No. 0.0006; Mismatches 0; Indels 0; Gaps 0;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 CCCCTTCCACTGGCTTTTGGAGAAAACAGCTGTCAGGCTTTCTGTATGCTTGT 624

DB 1 CCCCTTCCACTGGCTTTTGGAGAAAACAGCTGTCAGGCTTTCTGTATGCTTGT 60

Search completed: June 7, 2005, 22:14:33

Job time : 871.812 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 6, 2005, 10:37:53 ; Search time 60 seconds

(without alignments)  
1741.069 Million cell updates/sec

Title: US-10-071-174a-2

Score: 1084

Sequence: 1 MVDQLRETTMADPLERTE.....QAFSLCLTAFIYMTLL 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1035	95.5	184	1	BCL2_HUMAN
2	487	44.9	195	1	O99M66
3	474.5	43.8	191	1	BCL2_MOUSE
4	467.5	43.1	191	2	O7TPY8
5	217.5	20.1	179	2	O9ELF2
6	193.5	17.9	177	1	NR13_COTJA
7	188.5	17.4	177	2	O9QZNI
8	178.5	16.5	162	2	O9DH00
9	176.5	16.3	176	2	O8UWD5
10	174.5	16.1	172	2	O8U4D0
11	143.5	13.2	211	2	O9W6F1
12	131	12.1	192	2	O8HYU5
13	126	11.6	192	2	O8S043
14	125	11.5	174	2	O9W6F2
15	123	11.3	173	2	O9YKJ3
16	122	11.3	192	1	BAXA_BOVIN
17	122	11.3	350	2	O7YRZ9
18	121.5	11.2	188	2	O6GP82
19	121	11.2	192	1	BAXA_RAT
20	120	11.1	164	2	O70AD3
21	120	11.1	192	1	BAXA_HUMAN
22	118	10.9	239	2	O7SSV7
23	117	10.8	173	2	O8XJ2
24	117	10.8	192	1	BAXA_MOUSE
25	117	10.8	193	1	BCL2_MOUSE
26	117	10.8	229	1	BCL2_BOVIN
27	116	10.7	173	2	O8WZ49
28	116	10.7	235	2	O81008
29	115	10.6	192	2	O6A093
30	115	10.6	193	1	BCL2_MOUSE
31	114.5	10.6	238	2	O90Z98

32	113	10.4	114	2	O9NR76	O9NR76 homo sapien
33	113	10.4	143	1	BAXD_HUMAN	P55269 homo sapien
34	113	10.4	178	2	O8CFR2	O8CFR2 mus musculu
35	113	10.4	178	2	O9CYW5	O9CYW5 mus musculu
36	112.5	10.4	228	1	ARI_XENLA	O91827 xenopus lae
37	111.5	10.3	175	2	O925A9	O925A9 xenopus lae
38	111	10.2	193	2	O88996	O88996 rattus norv
39	111	10.2	219	2	O7TS60	O7TS60 rattus norv
40	111	10.2	350	2	O8HY55	O8HY55 canis famli
41	109	10.1	239	1	BCL2_HUMAN	P10415 homo sapien
42	108	10.0	228	2	O8UWD6	O8UWD6 brachydantio
43	107.5	9.9	192	2	O919N4	O919N4 brachydantio
44	107	9.9	193	2	O8CG14	O8CG14 mus musculu
45	107	9.9	350	1	MCCL_HUMAN	O07820 homo sapien

## ALIGNMENTS

RESULT 1  
BCL2\_HUMAN STANDARD; PRT; 194 AA.  
ID BCL2\_HUMAN  
AC O9HD36; O8TCS9;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Apoptosis regulator Bcl-2 (Bcl-2-like 10 protein) (Anti-apoptotic protein Nth).  
DE Name=BCL2L10; Synonym=BCL2;  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=21548034; PubMed=11689480; DOI=10.1093/hmg/10.21.2329;  
RA Zhang H., Holgrevet W., De Geyter C.;  
RT "Bcl-2, a novel anti-apoptotic member of the Bcl-2 family, blocks apoptosis in the mitochondria death pathway but not in the death receptor pathway."  
RT Hum. Mol. Genet. 10:2329-2339(2001).  
RL (2)  
RN SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=11278245; PubMed=11278245; DOI=10.1074/jbc.C000871200;  
RA Ke N., Godzik A., Reed J.C.;  
RT "Bcl-2, a novel Bcl-2 family member that differentially binds and regulates Bax and Bak."  
RL J. Biol. Chem. 276:12481-12484(2001).  
RN (3)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21477277; PubMed=11593390; DOI=10.1038/sj/onc.1204740;  
RA Aouache A., Arnaud E., Venet S., Lalle P., Gony M., Rigal D., Gillet G.;  
RT "Nth, a human homologue of Nr-13 associates with Bcl-2s and is an inhibitor of apoptosis."  
RL Oncogene 20:5846-5855(2001).  
CC -1- FUNCTION: Promotes cell survival. Suppresses apoptosis induced by BAX but not BAK.  
CC -1- SUBUNIT: Binds to Bcl-2, Bcl-X and BAX. Interacts with APAF-1.  
CC -1- SUBCELLULAR LOCATION: Associated with mitochondria and the nuclear envelope.  
CC -1- TISSUE SPECIFICITY: Widely expressed in adult tissues.  
CC -1- SIMILARITY: Expressed in the lungs, the liver and the kidneys.  
CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
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-----  
 CC EMBL, AF285092; AAG00503.1; ALT\_INIT.  
 DR EMBL, AF326964; AAK48715.1; ALT\_INIT.  
 DR EMBL, AJ458330; CAD30221.1; -.  
 DR Genew; HGNC:993; BCL2L10.  
 DR MIM; 606910; -.  
 DR GO; GO:0005624; C:membrane fraction; TAS.  
 DR GO; GO:0005515; P:protein binding; TAS.  
 DR GO; GO:0006916; P:anti-apoptosis; TAS.  
 DR GO; GO:0006915; P:apoptosis; TAS.  
 DR GO; GO:0006919; P:capase activation; TAS.  
 DR GO; GO:0007292; P:female gamete generation; TAS.  
 DR GO; GO:0007283; P:spermatogenesis; TAS.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR Pfam; PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1\_FALSE\_NEG.  
 DR PROSITE; PS01258; BH2; 1.  
 KW Apoptosis; Mitochondrion; Transmembrane.  
 FT DOMAIN 76 95 BH1.  
 FT DOMAIN 146 157 BH2.  
 FT TRANSMEM 173 190 Potential.  
 SQ SEQUENCE 194 AA; 21973 MW; 86F9F1A39377755F CRC64;

Query Match 95.5%; Score 1035; DB 1; Length 194;  
 Best Local Similarity 100.0%; Pred. No. 6,9e-89;  
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 MADPLRERTELLADYLGVCAREPPTPEAPSTPEAAVIRSAARLRQIHRSPFSAYIGY 70  
 DB 1 MADPLRERTELLADYLGVCAREPPTPEAPSTPEAAVIRSAARLRQIHRSPFSAYIGY 60  
 OY 71 PGNREELVALMADSVLSDSPPGTWGRVYTLVTFAGTLERGPVLYARWKMGFOPLRKEQ 130  
 DB 61 PGNREELVALMADSVLSDSPPGTWGRVYTLVTFAGTLERGPVLYARWKMGFOPLRKEQ 120  
 OY 131 EGDVARDCCORLVALLSSRLMGHRAMLQAGGMDGFCHEFRTPPLAFNRKOLVOAFISC 190  
 DB 121 EGDVARDCCORLVALLSSRLMGHRAMLQAGGMDGFCHEFRTPPLAFNRKOLVOAFISC 180  
 OY 191 LITTAFTYIMTRRL 204  
 DB 181 LITTAFTYIMTRRL 194  
 RESULT 2  
 O99M66 PRELIMINARY; PRT; 185 AA.  
 AC O99M66; 01-PUN-2001 (TREMBlrel. 17, Created)  
 DT 01-PUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-AR-2004 (TREMBlrel. 26, Last annotation update)  
 DE BCL2L10.  
 GN Name=Bcl2L10;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=22672518; PubMed=12787069;  
 RA Itoh T., Itoh A., Pleasure D.;  
 RT "Bcl-2-related protein family gene expression during oligodendroglial  
 RT differentiation";  
 RL J. Neurochem. 85:1500-1512(2003).  
 DR EMBL, AY028163; AAK31792.1; -.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.

DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR Pfam; PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 SQ SEQUENCE 185 AA; 21859 MW; 2EB9B94C8EC106A2 CRC64;

Query Match 44.9%; Score 487; DB 2; Length 185;  
 Best Local Similarity 46.4%; Pred. No. 1.5e-37;  
 Matches 89; Conservative 35; Mismatches 56; Indels 12; Gaps 2;

OY 11 MADPLRERTELLADYLGVCAREPPTPEAPSTPEAAVIRSAARLRQIHRSPFSAYIGY 70  
 DB 1 MEDPLQDRTRRLTFYILFCARAPPTPEPLPTVSVAALRRSVTSQIQEHODLFNSFRDY 60  
 OY 71 PGNREELVALMADSVLSDSPPGTWGRVYTLVTFAGTLERGPVLYARWKMGFOPLRKEQ 130  
 DB 61 QGNRLLELYQWADSLSDQSFNMGRLVLLAFVGTLMNDRYVRR-----RDQ 110  
 OY 131 EGD--VARDCCORLVALLSSRLMGHRAMLQAGGMDGFCHEFRTPPLAFNRKOLVOAF 188  
 DB 111 RNRLLERDCYLIYSLVNLRLTGRHSVLEAHGMDGFCQFFKNPLPGCFRRLLIRAIL 170  
 OY 189 SCLTTTAFIYLM 200  
 DB 171 SCFPAIAFYIM 182

RESULT 3  
 ID BCLB MOUSE STANDARD; PRT; 191 AA.  
 AC O920F3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Apoptosis regulator Bcl-B (Bcl-2-like 10 protein) (Anti-apoptotic  
 DE protein Bcl-2) (Bcl-2 homolog Diva).  
 GN Name=Bcl2L10; Synonyms=Bcl-2, Diva;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X DBA/2; TISSUE=Ovary;  
 RX MEDLINE=99094902; PubMed=9878060; DOI=10.1093/emboj/18.1.167;  
 RA Song Q.Z., Kuang Y.P., Dixit V.M., Vincenz C.;  
 RT "Bcl-2, a novel negative regulator of cell death, interacts with Apaf-  
 RT 1";  
 RL EMBO J. 18:167-178(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X DBA/2;  
 RX MEDLINE=99047617; PubMed=9829980; DOI=10.1074/jbc.273.49.32479;  
 RA Inohara N., Goutley T.S., Carrio R., Muniz M., Martino J., Garcia I.,  
 RA Koseki T., Hu Y., Chen S., Nunez G.;  
 RT "Diva, a Bcl-2 homologue that binds directly to Apaf-1 and induces  
 RT BH3-independent cell death";  
 RL J. Biol. Chem. 273:32479-32486(1998).  
 CC -1- FUNCTION: Promotes cell survival. Suppresses apoptosis.  
 CC -1- SUBUNIT: Binds to Bcl-2, Bcl-X and BAX. Interacts with APAF-1.  
 CC -1- SUBCELLULAR LOCATION: Associated with mitochondria and the nuclear  
 CC envelope (By similarity).  
 CC -1- TISSUE SPECIFICITY: Expressed in multiple embryonic tissues.  
 CC -1- RESTRICTED TO THE OVARY AND TESTIS IN ADULT MICE.  
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

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CC EMBL: AF102501; AAD08703.1; -  
 CC EMBL: AF067660; AAC63150.1; -  
 CC MGD: MGI:1330841; Bcl2l110.  
 DR GO: GO:0006916; P:anti-apoptosis; IDA.  
 DR GO: GO:0006915; P:apoptosis; IDA.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1\_FALSE\_NEG.  
 DR PROSITE: PS01258; BH2\_FALSE\_NEG.  
 DR Apoptosis; Mitochondrion; Transmembrane.  
 KM DOMAIN 79 98 BH1.  
 FT DOMAIN 144 155 BH2.  
 FT TRANSMEM 166 183 Potential.  
 SQ SEQUENCE 191 AA; 22302 MW; 819014E6B2DFE411 CRC64;

Query Match 43.8%; Score 474.5; DB 1; Length 191;  
 Best Local Similarity 48.2%; Pred. No. 2.3e-36;  
 Matches 94; Conservative 32; Mismatches 56; Indels 13; Gaps 3;

QY 13 DPLRRTLLADYGYCARPPTPEPAVLSAARLRQIHRSFSAVLGYPG 72  
 DB 6 DPLHRTLLSDYIFPCAREPDTPEPTVEALSLVTRQIOEHQEFSSFCESRG 65  
 QY 73 NRELVAMADSVSDSPGPTWGRVITLTFAGTLLEGPVLTARMKMGFGPRLKEQEG 132  
 DB 66 NRELVKMGADKXLSKODPFSWSQVLMIAFGLTMNGPVAVQXK-----DLG 116  
 QY 133 D---VARDCCRLVALLSRLMG-QHRAMLQAGGWDGCHFRPTFPPLAFMRKQVQVFL 188  
 DB 117 NRVITRCCCLIVNVLMLMGRRRLRLALGWDGCFRFPKPLPLGFWMLLIQVFL 176  
 QY 189 SCLLTAFIYMTWL 203  
 DB 177 SGFPATALFTWKRL 191

## RESULT 4

Q7TPY8 PRELIMINARY; PRT; 191 AA.  
 AC Q7TPY8;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Bcl2l10 protein.  
 DE Mus musculus (Mouse).  
 OS Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Egg;  
 RX MEDLINE=22388257; PubMed=1477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullaly S.J., Boeck S.A., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W., Vialation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S., Krzywicki M.I., Skalska U., Small D.E., Scherch A., Schein J.E., Jones S.J., Maira M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Egg;  
 RA Strausberg R.;  
 RX Submitted (May-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC052690; AAH52690.1; -  
 DR GO: GO:0016021; C:integral to membrane; TAS.  
 DR GO: GO:0006916; P:anti-apoptosis; IDA.  
 DR GO: GO:0006915; P:apoptosis; IDA.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 191 AA; 22230 MW; F2F176E6B0DE69A6 CRC64;

Query Match 43.1%; Score 467.5; DB 2; Length 191;  
 Best Local Similarity 47.7%; Pred. No. 1e-35;  
 Matches 93; Conservative 32; Mismatches 57; Indels 13; Gaps 3;

QY 13 DPLRRTLLADYGYCARPPTPEPAVLSAARLRQIHRSFSAVLGYPG 72  
 DB 6 DPLHRTLLSDYIFPCAREPDTPEPTVEALSLVTRQIOEHQEFSSFCESRG 65  
 QY 73 NRELVAMADSVSDSPGPTWGRVITLTFAGTLLEGPVLTARMKMGFGPRLKEQEG 132  
 DB 66 NRELVKMGADKXLSKODPFSWSQVLMIAFGLTMNGPVAVQXK-----DLG 116  
 QY 133 D---VARDCCRLVALLSRLMG-QHRAMLQAGGWDGCHFRPTFPPLAFMRKQVQVFL 188  
 DB 117 NRVITRCCCLIVNVLMLMGRRRLRLALGWDGCFRFPKPLPLGFWMLLIQVFL 176  
 QY 189 SCLLTAFIYMTWL 203  
 DB 177 SGFPATALFTWKRL 191

## RESULT 5

Q9ELP2 PRELIMINARY; PRT; 179 AA.  
 AC Q9ELP2;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE RSOEFL N13-like protein.  
 DE Name=RSORFL;  
 OS Meleagrid herpesvirus 1 (herpesvirus of turkeys).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Alphaherpesvirinae; Mardivirus.  
 NX NCBI\_TaxID=37108;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FC126;  
 RX MEDLINE=21195611; PubMed=11297687;  
 RA Kingham B.F., Zelnik V., Kopacek J., Majerciak V., Ney E., Schmidt C.J.;  
 RA "The genome of herpesvirus of turkeys: comparative analysis with RT Marek's disease viruses";  
 RT J. Gen. Virol. 82:1123-1135 (2001).  
 DR EMBL: AF282130; AAG30102.1; -  
 DR HSP; 007817; IR21.  
 DR GO: GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01258; BH2; UNKNOWN\_1.

SEQ SEQUENCE 179 AA; 19011 MW; A872B038A96D1823 CRC64;

Query Match 20.1%; Score 217.5; DB 2; Length 179;

Best Local Similarity 35.7%; Pred. No. 2.6e-12;

Matches 61; Conservative 14; Mismatches 55; Indels 41; Gaps 6;

OY 11 MADPLRERTELLADYLGVCAREPPTPEAPSTPEAAVLRSAARLRQIHRSFF--SAVL 68  
 DB 1 MADSLKETALLLEDFYFQHCCKEG---PPPS-PTAAELRRAAAELERRERPFPRSCAPL 56  
 OY 69 GYGNRFELVALMA-DSVLSDSFGPTGWRVTVLTFAGTL-----LERGPLVTARKK 119  
 DB 57 ASGGFQALSLAQSVASELNSGSGFRWGRCLATIVLGSGLATATLYENGCEBGP----- 109  
 OY 120 KMGFPRLKEGQGVARDCCRLVALLSSRLMGCHRAVLQAQSGMDGFCRFP 170  
 DB 110 -----SRLAALAAVLAEEGEMLEHGGMDGFCRFP 141

## RESULT 6

NR13\_COTUA

ID NR13\_COTUA STANDARD; PRT; 177 AA.

AC Q90343;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Apoptosis regulator NR-13.  
 GN Name=NR-13;  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Coturnix.  
 OX NCBI\_TaxID=93934;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryonic, and Neuroretina;  
 RX MEDLINE=95246730; PubMed=7729415;  
 RA Gillet G., Guerin M., Trembleau A., Brun G.;  
 RT "A Bcl-2-related gene is activated in avian cells transformed by the  
 RL Rous sarcoma virus".  
 RL Biochem. J. 141:1372-1381(1995).

CC -1- FUNCTION: Rous sarcoma virus-activated protein with anti-apoptotic  
 CC properties.  
 CC -1- SUBCELLULAR LOCATION: Plasma membrane.  
 CC -1- TISSUE SPECIFICITY: Mainly expressed in neural and muscular  
 CC tissues.  
 CC -1- DEVELOPMENTAL STAGE: Expression is dramatically down-regulated  
 CC after embryonic day 7 in the optic tectum, and correlates with the  
 CC onset of apoptosis in this area.  
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -----  
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 CC -----

DR EMBL; X84418; CAA59136.1; -.  
 DR HSSP; Q07817; IMAZ.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; Bcl2\_Family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 KW Apoptosis; Transmembrane.  
 FT DOMAIN 75 94 BH1.  
 FT DOMAIN 126 141 BH2.  
 FT TRANSMEM 86 106 Potential.

FT TRANSMEM 156 177 Potential.

SEQ SEQUENCE 177 AA; 18826 MW; ADSCE79D3353CCLF CRC64;

Query Match 17.9%; Score 193.5; DB 1; Length 177;

Best Local Similarity 33.1%; Pred. No. 4.5e-10;

Matches 57; Conservative 16; Mismatches 56; Indels 43; Gaps 6;

OY 11 MADPLRERTELLADYLGVCAREPPTPEAPSTPEAAVLRSAARLRQIHRSFFSAVL-- 68  
 DB 1 MGSLSKETALLLEDFYFQH--RAGGALPPSAT--AAELRRAAAELERRERPFPRSCAPL 56  
 OY 69 --GYGNRFELVALMADSVLSDSFGPTGWRVTVLTFAGTL-----LERGPLVTARKK 118  
 DB 57 ARAEPRBAALLRKVAALQLETDG--GLMWGRLLALVVFAGTLAAALAESACEBGP----- 109  
 OY 119 KMGFPRLKEGQGVARDCCRLVALLSSRLMGCHRAVLQAQSGMDGFCRFP 170  
 DB 110 -----SRLAALAAVLAEEGEMLEHGGMDGFCRFP 141

## RESULT 7

O902N1

ID O902N1 PRELIMINARY; PRT; 177 AA.

AC Q902N1;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Anti-apoptotic NR13.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC MEDLINE=22304624; PubMed=12133006; DOI=10.1042/BJ20020836;  
 RA Lalle P., Aouacheria A., Dumont-Miscopein A., Jamon M., Venet S.,  
 RA Bobichon H., Colas P., Deleage G., Geoujon C., Gillet G.;  
 RT "Evidence for crucial electrostatic interactions between Bcl-2  
 RL homology domains BH3 and BH4 in the anti-apoptotic Nr-13 protein.";  
 RL Biochem. J. 368:213-221(2002).

DR EMBL; AF375661; AAK54806.1; -.  
 DR HSSP; Q07817; IMAZ.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL2\_FAMILY; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 SEQ SEQUENCE 177 AA; 18778 MW; F06EF9C8B1AF250D CRC64;

Query Match 17.4%; Score 188.5; DB 2; Length 177;  
 Best Local Similarity 34.9%; Pred. No. 1.3e-09;  
 Matches 60; Conservative 12; Mismatches 57; Indels 43; Gaps 7;

OY 11 MADPLRERTELLADYLGVCAREPPTPEAPSTPEAAVLRSAARLRQIHRSFF--SAVL 68  
 DB 1 MGSLSKETALLLEDFYFQH--RAGGALPPSAT--AAELRRAAAELERRERPFPRSCAPL 56  
 OY 69 GYGNRFELVALM-ADSVLSDSFGPTGWRVTVLTFAGTL-----LERGPLVTARKK 118  
 DB 57 ARAEPR-BAALLRKVAALQLEAGGLMWGRLLALVVFAGTLAAALAESACEBGP----- 109  
 OY 119 KMGFPRLKEGQGVARDCCRLVALLSSRLMGCHRAVLQAQSGMDGFCRFP 170  
 DB 110 -----SRLAALAAVLAEEGEMLEHGGMDGFCRFP 141

## RESULT 8

O9DH00

ID O9DH00 PRELIMINARY; PRT; 162 AA.

AC O9DH00;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)



DT 01-MAR-2004 (TREMblrel. 26, last annotation update)  
 DE Myeloid cell leukemia protein MCL-1 (Fragment).  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99190706; PubMed=10090728;  
 RA Lee R.M., Gillet G., Burnside J., Thomas S.J., Neinan P.,  
 RT "Role of Nr13 in regulation of programmed cell death in the bursa of  
 RL Fabricius.";  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Soter L., Burnside J.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF120210; AAD31644.1; -;  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH; 1.  
 DR PROSITE; PS01258; BH2; UNKNOWN\_1.  
 DR NON\_TER  
 SQ SEQUENCE 211 AA; 23143 MW; A4B057C63F92BAC7 CRC64;

Query Match 13.2%; Score 143.5; DB 2; Length 211;  
 Best Local Similarity 28.5%; Pred. No. 2.7e-05;  
 Matches 53; Conservative 21; Mismatches 61; Indels 51; Gaps 9;

QY 13 DPLRRTRELLADYGYCARF-----PCTPEAPSTPEAAVRSAAAR 57  
 DB 16 DELRQESLELLRLRYREAAGEAPGVKLLPGILGGPGRGRASS---AVNEKLETLR 71  
 QY 58 QIHRSFSAV-LGYG-----NRELVALMADSVLSPGPT-WGRVTVLTVPAG 105  
 DB 72 RVGDGVQGHBLAFQGMRLKLEIKKEDDIAVCEVAQAQVFNQ--GVTNQGVVTLISF-- 127  
 QY 106 TLLRGPVLTAAWKWGFQPRLEQEGDVARDQORLVALLSRLMGQHRAMLAQGGWDG 165  
 DB 128 -----GAFPAKKLKS-----INQKCTIT---SLAGITTAIVSSKKEWLMSGGWDG 171  
 QY 166 FCHFR 171  
 DB 172 FVDFFR 177

RESULT 12  
 Q8HYU5 PRELIMINARY; PRT; 192 AA.  
 AC Q8HYU5;  
 DT 01-MAR-2003 (TREMblrel. 23, Created)  
 DT 01-MAR-2003 (TREMblrel. 23, last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, last annotation update)  
 DE Bax.  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yazawa M., Masuda K., Ohno K., Tsujimoto H.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB080230; BACS3619.1; -;  
 DR HSP; 007812; 1F16.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.

DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 SQ SEQUENCE 192 AA; 21299 MW; 7D3C326DDE62A87E CRC64;

Query Match 12.1%; Score 131; DB 2; Length 192;  
 Best Local Similarity 25.8%; Pred. No. 0.00035;  
 Matches 56; Conservative 29; Mismatches 70; Indels 62; Gaps 11;

QY 10 TMADELRRETELLADYGYCARFPG--TPP-PAPSTPEAAVLSAAARLQIHSFSA 66  
 DB 14 TSSQIMTKGALLLGFIQDRAGRGKGTPELPEQVQDASTKLSLCKRIQIDELDS- 72  
 QY 67 YLGYGNRFELVALMADSVLSDSPG-----TWGRVTVLTVPAGTLLERG 111  
 DB 73 -----NMEIQRMIA-AVDTSPREVFPRVALEMFSQGNFVGVALLFFASKLVKA 124  
 QY 112 -----PLVTAWKWGFQPRLEQEGDVARDQORLVALLSRLMGQHRAMLAQGGWDG 166  
 DB 125 LCTKVPELIRITMGW-----TLDFLRRLTG-----WIQDGGWDGL 161  
 QY 167 CHFFRTPEPLAFWKQVLAFLSLCTTAFTYLTWL 203  
 DB 162 LSYFGTP-----TW-QVTITFVAGVL-TASILTWKGM 191

## RESULT 13

Q8SQ43 PRELIMINARY; PRT; 192 AA.  
 AC Q8SQ43;  
 DT 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, last sequence update)  
 DT 01-JUN-2003 (TREMblrel. 24, last annotation update)  
 DE Bax-protein.  
 GN Name=bax;  
 OS Felis silvestris catus (Cat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamazaki J., Oguno K., Kano R., Hasegawa A.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB080724; BAB85810.1; -;  
 DR HSP; 007812; 1F16.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; BCL2\_FAMILY.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 SQ SEQUENCE 192 AA; 21283 MW; 852D271AB86923FB CRC64;

Query Match 11.6%; Score 126; DB 2; Length 192;

Best Local Similarity 25.8%; Pred. No. 0.001; Mismatches 70; Indels 62; Gaps 11;

QY 10 TMADELRRETELLADYGYCARFPG--TPP-PAPSTPEAAVLSAAARLQIHSFSA 66  
 DB 14 TSSQIMTKGALLLGFIQDRAGRGKGTPELPEQVQDASTKLSLCKRIQIDELDS- 72  
 QY 67 YLGYGNRFELVALMADSVLSDSPG-----TWGRVTVLTVPAGTLLERG 111  
 DB 73 -----NMEIQRMIA-AVDTSPREVFPRVALEMFSQGNFVGVALLFFASKLVKA 124  
 QY 112 -----PLVTAWKWGFQPRLEQEGDVARDQORLVALLSRLMGQHRAMLAQGGWDG 166  
 DB 125 LCTKVPELIRITMGW-----TLDFLRRLTG-----WIQDGGWDGL 161

QY 167 CHEFRTPEPLAFWRKQVLAFLSCLTTFATYLYMTRL 203  
 DB 162 LSYFGTP---TW--QVTYTFVAGVL-TASLTIWKKM 191

## RESULT 14

Q9W6F2 PRELIMINARY; PRT; 174 AA.  
 AC Q9W6F2;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Protein A1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archaeosuria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 CX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99190706; PubMed=10090728;  
 RA Lee R.M., Gillet G., Burnside J., Thomas S.J., Neilan P.;  
 RT "Role of Nr13 in regulation of programmed cell death in the bursa of  
 Fabricius";  
 RL Genes Dev. 13:718-728 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Sofer L., Burnside J.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF120211; AAD31645.1; -;  
 DR GO: GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
 DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
 SQ SEQUENCE 174 AA; 20095 MW; 4880F463DB2B352 CRC64;

Query Match 11.5%; Score 125; DB 2; Length 174;  
 Best Local Similarity 27.1%; Pred. No. 0.0012;  
 Matches 45; Conservative 33; Mismatches 58; Indels 30; Gaps 9;

QY 22 LADYLGICAREPGTPEPAPSTPEAVALRSAAARLQIHRSPFSAYLYGPGNRFELVAL- 80  
 DB 12 LAQDYLGVLQBSHL-GPA-QTRVAHVLRNINISLQDTEALRPFL---DRIDITSVD 65  
 QY 81 ----MADVLSLSD--SPGPT-MGRVVTLVTFAGTLBERGPIVYARWKKGQFOPRLKEQEGD 133  
 DB 66 VAKRIFNGVMERKPFADGNTNMGRIWITIFPGS-----LTKKLQEHGVLTGEKE-- 116  
 QY 134 VARDQRLVALLSRMGQHRAMLOAGGMD-GFCHFFRTPEPLAF 178  
 DB 117 -----KISYFITEYIINNKAMIDANGMGWGLTKFERRSPLSF 156

## RESULT 15

Q9JKL3 PRELIMINARY; PRT; 173 AA.  
 AC Q9JKL3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Bax protein splice variant k.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Jin K., He X., Greenberg D.A., Simon R.P., Graham S.H.;

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF235993; AAF36411.1; -;  
 DR HSBP; Q07812; I16.  
 DR GO: GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 SQ SEQUENCE 173 AA; 19661 MW; F19A45BCF642C34F CRC64;

Query Match 11.3%; Score 123; DB 2; Length 173;

Best Local Similarity 24.8%; Pred. No. 0.0018;  
 Matches 52; Conservative 26; Mismatches 62; Indels 70; Gaps 11;

QY 15 LRERTELLADYLGICAREPGTPE-PAPSTPEAVALRSAAARLQIHRSPFSAYLYGPGN 73  
 DB 12 IQDRAERNAE-----TPRLTLEQPPQDASTKGLSECLRIIDEL-----DN 53  
 QY 74 RPELVALMADSVLSDSPG-----TWGRVTVLVTFAGTLBERG-----PL 113  
 DB 54 NMELQRMVAD-VDTDSPREVFPRVADWPFADGNFMWGRVVALFYFASKLVLKALCTKYPR 112  
 QY 114 VTARKKKGFQPRLKEQEGDVARDQRLVALLSRMGQHRAMLOAGGMDGFCHFFRTPE 173  
 DB 113 LIRITGM-----TLDFLRERL---VWIDQGGMDGLSYFGTP 149  
 QY 174 FPLAFWRKQVLAFLSCLTTFATYLYMTRL 203  
 DB 150 -----TW--QVTYTFVAGVL-TASLTIWKKM 172

Search completed: June 6, 2005, 10:43:39  
 Job time : 62 sec

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## OM protein - protein search, using sw model

Run on: June 6, 2005, 10:39:24 ; Search time 42 Seconds

(without alignments)  
362,581 Million cell updates/sec

Title: US-10-071-174a-2

Perfect score: 1084  
Sequence: 1 MVDPLEKRTTADPLERTE.....QAFSLCLTTFATYVMTLL 204

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	11.2	192	1	US-08-112-208C-3 Sequence 3, Appli
2	121	11.2	192	1	US-08-248-819A-3 Sequence 3, Appli
3	121	11.2	192	2	US-08-337-646A-3 Sequence 3, Appli
4	121	11.2	192	2	US-08-856-531-3 Sequence 3, Appli
5	121	11.2	192	2	US-08-856-034-3 Sequence 3, Appli
6	121	11.2	192	3	US-08-927-326-3 Sequence 3, Appli
7	121	11.2	192	4	US-09-379-820A-3 Sequence 3, Appli
8	120	11.1	192	4	US-08-607-269-25 Sequence 25, Appli
9	120	11.1	192	1	US-08-471-058-13 Sequence 9, Appli
10	120	11.1	192	2	US-08-856-531-9 Sequence 9, Appli
11	120	11.1	192	2	US-08-856-034-9 Sequence 9, Appli
12	120	11.1	192	3	US-08-471-057-13 Sequence 13, Appli
13	120	11.1	192	3	US-09-127-048-7 Sequence 9, Appli
14	120	11.1	192	4	US-08-470-865-13 Sequence 13, Appli
15	120	11.1	192	4	US-09-155-327G-14 Sequence 14, Appli
16	120	11.1	192	5	PCT-US95-04600-25 Sequence 25, Appli
17	120	11.1	331	4	US-09-033-525-2 Sequence 2, Appli
18	119	11.0	192	1	US-08-112-208C-9 Sequence 9, Appli
19	119	11.0	192	1	US-08-248-819A-9 Sequence 9, Appli
20	119	11.0	192	2	US-08-337-646A-9 Sequence 9, Appli
21	119	11.0	192	4	US-08-927-326-9 Sequence 9, Appli
22	119	11.0	192	4	US-09-379-820A-9 Sequence 9, Appli
23	118	10.9	192	1	US-08-112-208C-2 Sequence 2, Appli
24	118	10.9	192	1	US-08-248-819A-2 Sequence 2, Appli
25	118	10.9	192	2	US-08-337-646A-2 Sequence 2, Appli
26	118	10.9	192	2	US-08-856-531-2 Sequence 2, Appli
27	118	10.9	192	2	US-08-856-034-2 Sequence 2, Appli

28	118	10.9	192	3	US-08-927-326-2 Sequence 2, Appli
29	118	10.9	192	4	US-09-379-820A-2 Sequence 2, Appli
30	117	10.8	192	1	US-08-112-208C-8 Sequence 8, Appli
31	117	10.8	192	1	US-08-248-819A-8 Sequence 8, Appli
32	117	10.8	192	2	US-08-337-646A-8 Sequence 8, Appli
33	117	10.8	192	2	US-08-856-531-8 Sequence 8, Appli
34	117	10.8	192	3	US-08-856-034-8 Sequence 8, Appli
35	117	10.8	192	3	US-09-127-048-6 Sequence 8, Appli
36	117	10.8	192	3	US-08-927-326-8 Sequence 8, Appli
37	117	10.8	192	4	US-09-379-820A-8 Sequence 8, Appli
38	117	10.8	193	4	US-09-155-327G-7 Sequence 7, Appli
39	117	10.8	193	4	US-09-949-016-10928 Sequence 10928, A
40	115	10.6	193	4	US-09-155-327G-9 Sequence 9, Appli
41	115	10.6	333	4	US-09-155-327G-10 Sequence 10, Appli
42	115	10.6	365	4	US-09-149-476-696 Sequence 696, App
43	115	10.6	365	4	US-09-010-147B-24 Sequence 24, Appli
44	112	10.3	192	1	US-08-798-897-6 Sequence 6, Appli
45	112	10.3	192	2	US-08-978-523-6 Sequence 6, Appli

## ALIGNMENTS

RESULT 1  
US-08-112-208C-3  
Sequence 3, Application US/08112208C  
Patent No. 5691179  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/112,208C  
FILING DATE: 26-AUG-1993  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURES:  
NAME/KEY: Protein  
LOCATION: 1..192  
OTHER INFORMATION: /note= "Protein sequence of murine  
US-08-112-208C-3  
OTHER INFORMATION: Bax."

Query Match 11.2%; Score 121; DB 1; Length 192;  
Best Local Similarity 26.7%; Pred. No. 5.8e-06;  
Matches 54; Conservative 22; Mismatches 64; Indels 62; Gaps 11;  
QY 23 LADYGYCARBGPPE-PAPSTPEAAVLSAARLQIHRSFSAVIGYQGNRRELVLM 81

Db 31 IODRAGNAGE--TELELEOPPODASTKLSCELRIGDELS-----NMELQMI 80  
Qy 82 ADVSLSDSGP-----TWGRVYTLVTFAGTLIERG-----PLVTARWKX 121  
Db 81 AD-VDRSDREVFVAVADMFDGFMNGRVVAFYFASKVLKXCTKVELRTINGW 139  
Qy 122 GFOPRLKEQEDVDARDCORLVALSSRLMGHRAWLQOQGMDCGCFEFTPEPLAFWRK 181  
Db 140 -----TIDFLERILG---WIDQGGWEGILSTYGTIP---TW-- 170  
Qy 182 QLVQAFSLCLTTAFIYLMTRL 203  
Db 171 QVTITFVAGVL-TASLTITWKX 191

RESULT 2  
US-08-248-819A-3  
Sequence 3, Application US/08248819A  
Patent No. 5700638  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew.  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/248, 819A  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..192  
OTHER INFORMATION: /note="Protein sequence of murine  
OTHER INFORMATION: Bax."  
US-08-248-819A-3

Query Match 11.2%; Score 121; DB 1; Length 192;  
Best Local Similarity 26.7%; Pred. No. 5.8e-06;  
Matches 54; Conservative 22; Mismatches 64; Indels 62; Gaps 11;

Qy 23 LADYLYGACRERGPE-PAPSTPEAAVLSAARLQIHRSPFSAYLYGPGNRFELVALM 81  
Db 31 IODRAGNAGE--TELELEOPPODASTKLSCELRIGDELS-----NMELQMI 80  
Qy 82 ADVSLSDSGP-----TWGRVYTLVTFAGTLIERG-----PLVTARWKX 121

Db 81 AD-VDRSDREVFVAVADMFDGFMNGRVVAFYFASKVLKXCTKVELRTINGW 139  
Qy 122 GFOPRLKEQEDVDARDCORLVALSSRLMGHRAWLQOQGMDCGCFEFTPEPLAFWRK 181  
Db 140 -----TIDFLERILG---WIDQGGWEGILSTYGTIP---TW-- 170  
Qy 182 QLVQAFSLCLTTAFIYLMTRL 203  
Db 171 QVTITFVAGVL-TASLTITWKX 191

RESULT 3  
US-08-337-646A-3  
Sequence 3, Application US/08337646A  
Patent No. 5856171  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,646A  
FILING DATE: 10-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248, 819  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000620  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..192  
OTHER INFORMATION: /note="Protein sequence of murine  
OTHER INFORMATION: Bax."  
US-08-337-646A-3

Query Match 11.2%; Score 121; DB 2; Length 192;  
Best Local Similarity 26.7%; Pred. No. 5.8e-06;  
Matches 54; Conservative 22; Mismatches 64; Indels 62; Gaps 11;

Qy 23 LADYLYGACRERGPE-PAPSTPEAAVLSAARLQIHRSPFSAYLYGPGNRFELVALM 81  
Db 31 IODRAGNAGE--TELELEOPPODASTKLSCELRIGDELS-----NMELQMI 80  
Qy 82 ADVSLSDSGP-----TWGRVYTLVTFAGTLIERG-----PLVTARWKX 121

Db 81 AD-VDROSPREVFPRVAADMFADGNFMNGRVVALLFYFASKVLKALCTKPELIRITMGW 139  
Qy 122 GFQRLKEQBGDVARDQRLVALLSSRLMGHRAMLAQGGWDGCFHFRTPPLAFYRK 181  
Db 140 -----TLDFLRERLLG-----WIDQGGMEGLSYFGTP-----TW-- 170  
Qy 182 QLVQAFSLCLTTAFIYLMTRL 203  
Db 171 QTVTIFVAGVL-TASLTIWKKM 191

## RESULT 4

US-08-856-531-3  
; Sequence 3, Application US/08856531  
; Patent No. 5942490  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: CELL DEATH REGULATORS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howell & Hafeerkamp, L.C.  
; STREET: 7733 Foreyth Blvd., Suite 1400  
; CITY: St. Louis  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,531  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, Donald R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 976176  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..192  
; OTHER INFORMATION: /note= "Murine BAX polypeptide"  
; US-08-856-531-3

Query Match 11.2%; Score 121; DB 2; Length 192;  
Best Local Similarity 26.7%; Pred. No. 5.8e-06;  
Matches 54; Conservative 22; Mismatches 64; Indels 62; Gaps 11;  
Qy 23 LADYLGYCARPGPE-PAPSTPEAAVIRSAARLRQIHRSFFSAIYLGYPGNRFELVALM 81  
Db 31 IQDRAGRWAGE--TPELTLEQPPQDASTKSLSECLRRIGDELDS-----NMELQPMI 80  
Qy 82 ADVSLDSPGPD-----TWGRVTVLTFAAGTLLERG-----PLVYARMWKW 121  
Db 81 AD-VDROSPREVFPRVAADMFADGNFMNGRVVALLFYFASKVLKALCTKPELIRITMGW 139  
Qy 122 GFQRLKEQBGDVARDQRLVALLSSRLMGHRAMLAQGGWDGCFHFRTPPLAFYRK 181  
Db 140 -----TLDFLRERLLG-----WIDQGGMEGLSYFGTP-----TW-- 170  
Qy 182 QLVQAFSLCLTTAFIYLMTRL 203  
Db 171 QTVTIFVAGVL-TASLTIWKKM 191

Db 171 QTVTIFVAGVL-TASLTIWKKM 191

## RESULT 5

US-08-856-034-3  
; Sequence 3, Application US/08856034  
; Patent No. 5955595  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: CELL DEATH REGULATORS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howell & Hafeerkamp, L.C.  
; STREET: 7733 Foreyth Blvd., Suite 1400  
; CITY: St. Louis  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,034  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, Donald R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 976175  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..192  
; OTHER INFORMATION: /note= "Murine BAX polypeptide"  
; US-08-856-034-3

Query Match 11.2%; Score 121; DB 2; Length 192;  
Best Local Similarity 26.7%; Pred. No. 5.8e-06;  
Matches 54; Conservative 22; Mismatches 64; Indels 62; Gaps 11;  
Qy 23 LADYLGYCARPGPE-PAPSTPEAAVIRSAARLRQIHRSFFSAIYLGYPGNRFELVALM 81  
Db 31 IQDRAGRWAGE--TPELTLEQPPQDASTKSLSECLRRIGDELDS-----NMELQPMI 80  
Qy 82 ADVSLDSPGPD-----TWGRVTVLTFAAGTLLERG-----PLVYARMWKW 121  
Db 81 AD-VDROSPREVFPRVAADMFADGNFMNGRVVALLFYFASKVLKALCTKPELIRITMGW 139  
Qy 122 GFQRLKEQBGDVARDQRLVALLSSRLMGHRAMLAQGGWDGCFHFRTPPLAFYRK 181  
Db 140 -----TLDFLRERLLG-----WIDQGGMEGLSYFGTP-----TW-- 170  
Qy 182 QLVQAFSLCLTTAFIYLMTRL 203  
Db 171 QTVTIFVAGVL-TASLTIWKKM 191

Db 171 QTVTIFVAGVL-TASLTIWKKM 191

## RESULT 6

US-08-927-326-3  
; Sequence 3, Application US/08927326  
; Patent No. 6184202  
; GENERAL INFORMATION:

APPLICANT: KORMSEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,326  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,646  
FILING DATE: 10-NOV-1994  
APPLICATION NUMBER: US 08/248,819  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000620  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: 326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..192  
OTHER INFORMATION: /note="Protein sequence of murine  
OTHER INFORMATION: Bax."  
US-08-927-326-3  
Query Match 11.2%; Score 121; DB 3; Length 192;  
Best Local Similarity 26.7%; Pred. No. 5.8e-06;  
Matches 54; Conservative 22; Mismatches 64; Indels 62; Gaps 11;  
QY 23 LADYGYCARPGTPE-PAPSTPEAAVLRSAARLRQIHRSFFSAVLGPGRRFLVALM 81  
DB 31 IQDRAGRWAGE--TPELTLEBPPODASTKSLSECLRRIGDELDS-----NMELQRM 80  
QY 82 ADSVLSDSGPG-----TWGRVYTVTFPGTLLERG-----PLVTARMKKM 121  
DB 81 AD-VDRDSPREVFRVADMPADGNFMNGRVVALTFYFASKVLVXALCTKVPFLRTIMGW 139  
QY 122 GFQRLKEQEGDVARDQRLVALLSRMLGQHRAMVLAQGGMDGCFHFRTPPLAFWRK 181  
DB 140 -----TLDPLERLLG---WIDQGGWEGLLSYGTF---TW-- 170  
QY 182 QLVQAFSLCLTTAFIYLMTRL 203  
DB 171 QVTTFVAGVL-TASLTIMKKM 191  
RESULT 7  
US-09-379-820A-3  
Sequence 3, Application US/09379820A  
Patent No. 6500626

GENERAL INFORMATION:  
APPLICANT: Kormseier, Stanley J.  
TITLE OF INVENTION: Cell Death Regulator  
FILE REFERENCE: 6029-1314  
CURRENT APPLICATION NUMBER: US/09/379,820A  
CURRENT FILING DATE: 1999-08-24  
PRIOR APPLICATION NUMBER: 08/856,034  
PRIOR FILING DATE: 1997-05-14  
NUMBER OF SEQ ID NOS: 32  
SEQ ID NO 3  
LENGTH: 192  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-379-820A-3  
Query Match 11.2%; Score 121; DB 4; Length 192;  
Best Local Similarity 26.7%; Pred. No. 5.8e-06;  
Matches 54; Conservative 22; Mismatches 64; Indels 62; Gaps 11;  
QY 23 LADYGYCARPGTPE-PAPSTPEAAVLRSAARLRQIHRSFFSAVLGPGRRFLVALM 81  
DB 31 IQDRAGRWAGE--TPELTLEBPPODASTKSLSECLRRIGDELDS-----NMELQRM 80  
QY 82 ADSVLSDSGPG-----TWGRVYTVTFPGTLLERG-----PLVTARMKKM 121  
DB 81 AD-VDRDSPREVFRVADMPADGNFMNGRVVALTFYFASKVLVXALCTKVPFLRTIMGW 139  
QY 122 GFQRLKEQEGDVARDQRLVALLSRMLGQHRAMVLAQGGMDGCFHFRTPPLAFWRK 181  
DB 140 -----TLDPLERLLG---WIDQGGWEGLLSYGTF---TW-- 170  
QY 182 QLVQAFSLCLTTAFIYLMTRL 203  
DB 171 QVTTFVAGVL-TASLTIMKKM 191  
RESULT 8  
US-08-607-269-25  
Sequence 25, Application US/08607269  
Patent No. 5702897  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
TITLE OF INVENTION: Interaction of Proteins Involved in a  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/607,269  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/226,876  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-1J 9882  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-8901  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-607-269-25

Query Match 11.1%; Score 120; DB 1; Length 192;  
Best Local Similarity 25.3%; Pred. No. 7.7e-06;  
Matches 55; Conservative 29; Mismatches 71; Indels 62; Gaps 11;

QY 10 TMAPLRLRETELLADYLYGCAREPG--TPPEA-PSPEAAVLRSAAARLQIHSFSPA 66  
DB 14 TSSEQIMTKGALLGFIODRAGRWGAPALADPVQDASTKKLSCLKRIGDELDS- 72  
QY 67 YLGRGNRFEVLAMADSVLSDSPG-----TWGRVTVLTVPAGTLLERG 111  
DB 73 -----NMEIQRMIA-AVDTDSPREVFPRVAADMFSDGNFMWGVVALFYFASKLVIKA 124  
QY 112 -----PLVTARWKKKGFPRLKEGEGDVARDCCQLVALLSRLMGHRAWLQAQGMDF 166  
DB 125 LCTKVPFLIRITMG-----TLDFLRRLIG---WIODQGMDF 161  
QY 167 CHFFTPPEPLAFWRKQLVQAFSLCLTTAFIYLTWL 203  
DB 162 LSYRGT-----TW-QVTYIFVAGVL-TASLTITKMM 191

## RESULT 9

US-08-471-058-13  
Sequence 13, Application US/08471058  
Patent No. 5770443

## GENERAL INFORMATION:

APPLICANT: Kiefer, Michael C.

APPLICANT: Barr, Philip J.

TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING

TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Pasteo for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471.058

FILING DATE: 06-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/320,157

FILING DATE: 07-OCT-1994

APPLICATION NUMBER: 08/160,067

FILING DATE: 30-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20007.12

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-813-5600

TELEFAX: 415-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-471-058-13

Query Match 11.1%; Score 120; DB 1; Length 192;  
Best Local Similarity 25.3%; Pred. No. 7.7e-06;  
Matches 55; Conservative 29; Mismatches 71; Indels 62; Gaps 11;

QY 10 TMAPLRLRETELLADYLYGCAREPG--TPPEA-PSPEAAVLRSAAARLQIHSFSPA 66  
DB 14 TSSEQIMTKGALLGFIODRAGRWGAPALADPVQDASTKKLSCLKRIGDELDS- 72  
QY 67 YLGRGNRFEVLAMADSVLSDSPG-----TWGRVTVLTVPAGTLLERG 111  
DB 73 -----NMEIQRMIA-AVDTDSPREVFPRVAADMFSDGNFMWGVVALFYFASKLVIKA 124  
QY 112 -----PLVTARWKKKGFPRLKEGEGDVARDCCQLVALLSRLMGHRAWLQAQGMDF 166  
DB 125 LCTKVPFLIRITMG-----TLDFLRRLIG---WIODQGMDF 161  
QY 167 CHFFTPPEPLAFWRKQLVQAFSLCLTTAFIYLTWL 203  
DB 162 LSYRGT-----TW-QVTYIFVAGVL-TASLTITKMM 191

## RESULT 10

US-08-856-531-9  
Sequence 9, Application US/08856531  
Patent No. 5942490

## GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: CELL DEATH REGULATORS

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howell & Haferkamp, L.C.

STREET: 7733 Foreyn Blvd., Suite 1400

CITY: St. Louis

STATE: MO

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856,531

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, Donald R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-6092

TELEFAX: 314-727-5188

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..192

OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-856-531-9

Query Match 11.1%; Score 120; DB 2; Length 192;  
Best Local Similarity 25.3%; Pred. No. 7.7e-06;  
Matches 55; Conservative 29; Mismatches 71; Indels 62; Gaps 11;

QY 10 TMAPLRLRETELLADYLYGCAREPG--TPPEA-PSPEAAVLRSAAARLQIHSFSPA 66  
DB 14 TSSEQIMTKGALLGFIODRAGRWGAPALADPVQDASTKKLSCLKRIGDELDS- 72  
QY 67 YLGRGNRFEVLAMADSVLSDSPG-----TWGRVTVLTVPAGTLLERG 111  
DB 73 -----NMEIQRMIA-AVDTDSPREVFPRVAADMFSDGNFMWGVVALFYFASKLVIKA 124  
QY 112 -----PLVTARWKKKGFPRLKEGEGDVARDCCQLVALLSRLMGHRAWLQAQGMDF 166  
DB 125 LCTKVPFLIRITMG-----TLDFLRRLIG---WIODQGMDF 161  
QY 167 CHFFTPPEPLAFWRKQLVQAFSLCLTTAFIYLTWL 203  
DB 162 LSYRGT-----TW-QVTYIFVAGVL-TASLTITKMM 191

Db 14 TSSBOIMTKGALLLGFIODRAGRMGGAPELALDPVPODASTKKLSGKRIIGBELDS- 72  
Qy 67 YLGGNRPFLVALMADSVLSDSPGP-----TWGRVVTLVTFAGTLLBERG 111  
Db 73 -----NMELORMIA-AVDITSPREVFPRVAADMFSDGNFMWGRVVALFYFASKLVYKA 124  
Qy 112 -----PLVTARKKKWGFPRLKEQBGDVARDCCRLVALLSRLMGQHRAMLOAGGWDGF 166  
Db 125 LCTKVPBELRTIMGN-----TLDFLRERLLG-----WIDQGQGMDDL 161  
Qy 167 CHFRTPPLAFWRKQLOVAFISCLTTAFIYLTREL 203  
Db 162 LSYFGTP-----TW--QVTITFVAGVL-TASLTIWKKM 191

## RESULT 11

US-08-856-034-9  
; Sequence 9, Application US/08856034  
; Patent No. 5955595  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: CELL DEATH REGULATORS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howell & Haferkamp, L.C.  
; STREET: 7733 Foreyth Blvd., Suite 1400  
; CITY: St. Louis  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,034  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, Donald R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 976175  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..192  
; OTHER INFORMATION: /note= "Human BAX polypeptide"  
US-08-856-034-9

Query Match 11.1%; Score 120; DB 2; Length 192;  
Best Local Similarity 25.3%; Pred. No. 7.7e-06;  
Matches 55; Conservative 29; Mismatches 71; Indels 62; Gaps 11;  
Qy 10 TMADPLRRTTELLADYIGCARBEG--TPBPA-PTBPAVLRSAAARLQIHRSFSPA 66  
Db 14 TSSBOIMTKGALLLGFIODRAGRMGGAPELALDPVPODASTKKLSGKRIIGBELDS- 72  
Qy 67 YLGGNRPFLVALMADSVLSDSPGP-----TWGRVVTLVTFAGTLLBERG 111  
Db 73 -----NMELORMIA-AVDITSPREVFPRVAADMFSDGNFMWGRVVALFYFASKLVYKA 124  
Qy 112 -----PLVTARKKKWGFPRLKEQBGDVARDCCRLVALLSRLMGQHRAMLOAGGWDGF 166

Db 125 LCTKVPBELRTIMGN-----TLDFLRERLLG-----WIDQGQGMDDL 161  
Qy 167 CHFRTPPLAFWRKQLOVAFISCLTTAFIYLTREL 203  
Db 162 LSYFGTP-----TW--QVTITFVAGVL-TASLTIWKKM 191

## RESULT 12

US-08-471-057-13  
; Sequence 13, Application US/08471057  
; Patent No. 6015687  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,057  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/320,157  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007, 20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-471-057-13

Query Match 11.1%; Score 120; DB 3; Length 192;  
Best Local Similarity 25.3%; Pred. No. 7.7e-06;  
Matches 55; Conservative 29; Mismatches 71; Indels 62; Gaps 11;  
Qy 10 TMADPLRRTTELLADYIGCARBEG--TPBPA-PTBPAVLRSAAARLQIHRSFSPA 66  
Db 14 TSSBOIMTKGALLLGFIODRAGRMGGAPELALDPVPODASTKKLSGKRIIGBELDS- 72  
Qy 67 YLGGNRPFLVALMADSVLSDSPGP-----TWGRVVTLVTFAGTLLBERG 111  
Db 73 -----NMELORMIA-AVDITSPREVFPRVAADMFSDGNFMWGRVVALFYFASKLVYKA 124  
Qy 112 -----PLVTARKKKWGFPRLKEQBGDVARDCCRLVALLSRLMGQHRAMLOAGGWDGF 166  
Db 125 LCTKVPBELRTIMGN-----TLDFLRERLLG-----WIDQGQGMDDL 161  
Qy 167 CHFRTPPLAFWRKQLOVAFISCLTTAFIYLTREL 203  
Db 162 LSYFGTP-----TW--QVTITFVAGVL-TASLTIWKKM 191

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RESULT 13
US-09-127-048-7
; Sequence 7, Application US/09127048
; Patent No. 6165732
; GENERAL INFORMATION:
; APPLICANT: Koremeyer, Stanley J.
; APPLICANT: Schlesinger, Paul H.
; TITLE OR INVENTION: Method for identifying Apoptosis Modulating Compounds
; FILE REFERENCE: 6029-6052
; CURRENT APPLICATION NUMBER: US/09/127,048
; CURRENT FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: 60/061,823
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-127-048-7

Query Match      11.1%; Score 120; DB 3; Length 192;
Beat Local Similarity 25.3%; Pred. No. 7, 7e-06;
Matches 55; Conservative 29; Mismatches 71; Indels 62; Gaps 11

Cy      10 TMADPLRRTTELLADYIGYCAREG--TPPEA-ESTPEAVLRSAARLRQIHHSFSA 66
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      67 YLGYGNRFFELVALMADSVLSPSPG-----TWGRVYTLVTFAGTLLERG 111
      73 -----NMEIORMIA-AVDTDSPREVFPRVAADMFSDGNFVNGRVALLFTASKLVKA 124
      112 -----PLVTARWKKKGFQPRLKEGEGDYARDQRLVALLSSRLMGQHRAMLQAQSGWDF 166
      125 LCTKVPRLIRITMGM-----TLDFLREHLTG-----WIDQSGMGL 161
      167 CFFRTPPPLAFWRKQLVQAFISCLLTFAFYLMTRL 203
      162 LSYFGTP---TW-QTVTIFVAGVL-TASLTIWKKM 191

Db
162 LSYFGTP---TW-QTVTIFVAGVL-TASLTIWKKM 191

RESULT 14
US-08-470-865-13
; Sequence 13, Application US/08470865
; Patent No. 6586395
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP U.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & ROEBSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,865
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.

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[illegible]

Db :| |  
162 LSYFSTP---TW--QVTIIFVAGVL-TASLTITWKM 191

Search completed: June 6, 2005, 10:45:12  
Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: June 6, 2005, 10:41:39 ; Search time 53 Seconds  
(without alignments)  
1330.542 Million cell updates/sec

Title: US-10-071-174A-2

Perfect score: 1084  
Sequence: 1 MVDQLRERTMADPLRERTE.....QAFISCLLTAFIVMTRELL 204

## Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
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19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1084	100.0	204	14	US-10-071-174-2
2	701	66.7	130	9	US-09-912-599-7
3	328.5	30.3	141	9	US-09-764-847-800
4	328.5	30.3	141	14	US-10-092-154-800
5	153	14.1	30	14	US-10-071-174-19
6	128	11.8	24	14	US-10-071-174-13
7	121	11.2	191	14	US-10-196-793A-46
8	120	11.1	192	14	US-10-101-482-13
9	120	11.1	192	14	US-10-277-693A-9
10	120	11.1	192	14	US-10-306-878-5
11	120	11.1	192	15	US-10-421-285-10
12	120	11.1	331	9	US-09-033-525-2
13	120	11.1	331	17	US-10-640-668-2

14	118	10.9	23	9	US-09-912-599-14	Sequence 14, Appli
15	118	10.9	192	14	US-10-277-693A-2	Sequence 2, Appli
16	117	10.8	192	14	US-10-277-693A-8	Sequence 8, Appli
17	117	10.8	192	15	US-10-421-285-8	Sequence 8, Appli
18	117	10.8	192	16	US-10-451-467A-2	Sequence 7, Appli
19	117	10.8	193	9	US-09-925-674A-7	Sequence 6, Appli
20	117	10.8	193	16	US-10-450-166-6	Sequence 9, Appli
21	115	10.6	193	9	US-09-925-674A-9	Sequence 696, App
22	115	10.6	365	10	US-09-809-191-696	Sequence 696, App
23	115	10.6	365	10	US-09-882-171-696	Sequence 696, App
24	115	10.6	365	15	US-10-164-861-696	Sequence 696, App
25	114	10.5	21	14	US-10-071-174-6	Sequence 6, Appli
26	113	10.4	18	14	US-10-071-174-11	Sequence 31, Appli
27	112	10.3	237	16	US-10-659-705-5	Sequence 5, Appli
28	111	10.2	21	14	US-10-071-174-3	Sequence 3, Appli
29	111	10.2	192	14	US-10-277-693A-3	Sequence 3, Appli
30	111	10.2	239	15	US-10-148-953A-5	Sequence 5, Appli
31	110.5	10.2	152	14	US-10-158-769-2	Sequence 2, Appli
32	110	10.1	239	15	US-10-148-953A-3	Sequence 3, Appli
33	109	10.1	239	8	US-08-726-211-5	Sequence 5, Appli
34	109	10.1	239	10	US-09-993-420A-8	Sequence 8, Appli
35	109	10.1	239	14	US-10-277-693A-10	Sequence 10, Appli
36	109	10.1	239	14	US-10-141-618-12	Sequence 12, Appli
37	109	10.1	239	14	US-10-053-645A-21	Sequence 21, Appli
38	109	10.1	239	15	US-10-387-961A-5	Sequence 5, Appli
39	109	10.1	239	15	US-10-003-632C-1	Sequence 1, Appli
40	109	10.1	239	15	US-10-003-632C-3	Sequence 3, Appli
41	109	10.1	239	15	US-10-003-632C-10	Sequence 10, Appli
42	109	10.1	239	15	US-10-003-632C-13	Sequence 13, Appli
43	109	10.1	239	15	US-10-148-953A-1	Sequence 1, Appli
44	109	10.1	239	15	US-10-148-953A-2	Sequence 2, Appli
45	109	10.1	239	15	US-10-148-953A-4	Sequence 4, Appli

## ALIGNMENTS

RESULT 1									
US-10-071-174-2									
; Sequence 2, Application US/10071174									
; Publication No. US20030176671A1									
; GENERAL INFORMATION:									
; APPLICANT: REED, JOHN C.									
; APPLICANT: KE, NING									
; APPLICANT: GODDIX, ADAM									
; TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-2 AND METHODS FOR MAKING AND									
; FILE REFERENCE: 087102-0272558									
; CURRENT APPLICATION NUMBER: US/10/071,174									
; CURRENT FILING DATE: 2002-02-07									
; PRIOR APPLICATION NUMBER: 60/267,166									
; NUMBER OF SEQ ID NOS: 36									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 2									
; LENGTH: 204									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-071-174-2									
Query Match									
Best Local Similarity 100.0%; Score 1084; DB 14; Length 204;									
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	MVDQLRERTMADPLRERTE		1	MVDQLRERTMADPLRERTE		60		
QY	61	RSFSAVYIGYGNRELV		61	RSFSAVYIGYGNRELV		120		
DB	61	RSFSAVYIGYGNRELV		61	RSFSAVYIGYGNRELV		120		
QY	121	WQFGRLEKQEGDVARD		121	WQFGRLEKQEGDVARD		180		

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Db      121 WFFQRLKEQEGDVARDCCRLVALLSRLMGQHRAMLQAGGMDGFCFFRTPPFLAFWR 180
Qy      181 KOLVQAFISCLTTPAFIYLMTRL 204
Db      181 KOLVQAFISCLTTPAFIYLMTRL 204

RESULT 2
US-09-912-599-7
; Sequence 7, Application US/09912599
; Patent No. US20020106731A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Bcl-2-like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO44P1
; CURRENT APPLICATION NUMBER: US/09/912,599
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/03080
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/179,487
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/180,697
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-599-7

Query Match      64.7%; Score 701; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 7.5e-64;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      75 FELVALMDSVLSDSPGPTWGRVTVLTFPAGTLLERGPLVTARMKMGFQPLKQEGDV 134
Db      1 FELVALMDSVLSDSPGPTWGRVTVLTFPAGTLLERGPLVTARMKMGFQPLKQEGDV 60

Qy      135 ARDCORVALLSRLMGQHRAMLQAGGMDGFCFFRTPPFLAFWRKOLVQAFISCLTTP 194
Db      61 ARDCORVALLSRLMGQHRAMLQAGGMDGFCFFRTPPFLAFWRKOLVQAFISCLTTP 120

Qy      195 AFYIYLMTRL 204
Db      121 AFYIYLMTRL 130

RESULT 3
US-09-764-847-800
; Sequence 800, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 800
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (86)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (108)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-847-800

Query Match      30.3%; Score 328.5; DB 9; Length 141;
Best Local Similarity 67.0%; Pred. No. 1.5e-25;
Matches 67; Conservative 1; Mismatches 11; Indels 21; Gaps 2;

Qy      90 PGPTWGRVTVLTFPAGTLLERGPLVTARMKMGFQPLKQEGDVARDCCORVALLSRL 149
Db      40 PRPHLGRVTVLTFPAGTLLERGPLVTARMKMGFQPLKQEGDVARDCCORVALLSRL 99

Qy      150 MGOHRA-----WLAQGGMDG-FCH 168
Db      100 MGOHRRPGCKLRAGMAFVTSAGPPFHWLFGENSMGRLCFH 139

RESULT 4
US-10-092-154-800
; Sequence 800, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 800
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (86)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (108)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-092-154-800

Query Match      30.3%; Score 328.5; DB 14; Length 141;
Best Local Similarity 67.0%; Pred. No. 1.5e-25;
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Matches 67; Conservative 1; Mismatches 11; Indels 21; Gaps 2;

Qy 90 RPPWGRVTVTFTGTLLEKGLVTARWKKGFQPLKEGSDVARDQRLVALLSRL 149  
Db 40 PRPHGRVTVTFTGTLLEKGLVTARWKKGFQPLKEGSDVARDQRLVALLSRL 99  
Qy 150 MGOHRA-----WLOAGGMDG-FCH 168  
Db 100 MGOHRA-----WLOAGGMDG-FCH 139

RESULT 5  
US-10-071-174-19  
; Sequence 19, Application US/10071174  
; Publication No. US20030176671A1  
; GENERAL INFORMATION:  
; APPLICANT: REED, JOHN C.  
; APPLICANT: KE, NING  
; APPLICANT: GODZIK, ADAM  
; TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND  
; TITLE OF INVENTION: USING SAME  
; FILE REFERENCE: 087102-0272558  
; CURRENT APPLICATION NUMBER: US/10/071,174  
; PRIOR FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 60/267,166  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-071-174-19

Query Match 14.1%; Score 153; DB 14; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.3e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MADSVLSDSPGPTWGRVTVTFTGTLLEK 30

RESULT 6  
US-10-071-174-13  
; Sequence 13, Application US/10071174  
; Publication No. US20030176671A1  
; GENERAL INFORMATION:  
; APPLICANT: REED, JOHN C.  
; APPLICANT: KE, NING  
; APPLICANT: GODZIK, ADAM  
; TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND  
; TITLE OF INVENTION: USING SAME  
; FILE REFERENCE: 087102-0272558  
; CURRENT APPLICATION NUMBER: US/10/071,174  
; PRIOR FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 60/267,166  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-071-174-13

Query Match 11.8%; Score 128; DB 14; Length 24;  
Best Local Similarity 100.0%; Pred. No. 6.6e-06;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LRRETELLADYLGVCAREPGTPE 38  
Db 1 LRRETELLADYLGVCAREPGTPE 24

RESULT 7  
US-10-196-793A-46  
; Sequence 46, Application US/10196793A  
; Publication No. US20030086919A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENBLUM, MARTIN G.  
; APPLICANT: LIU, YIYING  
; TITLE OF INVENTION: THERAPEUTIC AGENTS COMPRISING PRO-APOPTOTIC PROTEINS  
; FILE REFERENCE: CLFR:01205  
; CURRENT APPLICATION NUMBER: US/10/196,793A  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 60/360,361  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/332,886  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 60/306,091  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-196-793A-46

Query Match 11.2%; Score 121; DB 14; Length 191;  
Best Local Similarity 27.4%; Pred. No. 0.00045;  
Matches 58; Conservative 29; Mismatches 73; Indels 52; Gaps 12;

Qy 10 TMADPLRRTRELLADYLGVCAREPG--TPRPA-PTTEAAVLSAARLQIHSPSA 66  
Db 13 TSSQIMTGTALLLGFTQDRAGRWGEPALADPVQDASTYKLSCLKRIIDELDS 71  
Qy 67 YLGPNGNFEVLVAMADSVLSDSPG-----TWGRVTVTFTGTLLEK 111  
Db 72 -----NMELORMIA-AVDIDSPREVFRAADMFSDGNWGRVVALFFPASTLVYKA 123  
Qy 112 PLVTARWKKWGPQPLKEGSDVARDQRLVALLSSRLMGHRAWLOAGGMDGFCHEFR 171  
Db 124 -LVTK-----VPEL-----IRTMGTLDPLREIRLLG---WIDQGGMDGLSYFG 165  
Qy 172 TFPPLAFWKOLVQAFSLCLTTAFIYIWTBL 203  
Db 166 TP---TW--QVTTFVAGVL-TASLTIWKKM 190

RESULT 8  
US-10-101-482-13  
; Sequence 13, Application US/10101482  
; Publication No. US2003008837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; APPLICANT: KIEFER, PHILIP J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/101,482  
; FILING DATE: 18-Mar-2002

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? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/320,157
? FILING DATE: 07-OCT-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: LEHNHARDT, SUSAN K.
? REGISTRATION NUMBER: 33,943
? REFERENCE/DOCKET NUMBER: 23647-20007.20
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 813-5600
? TELEFAX: (415) 494-0792
? TELEX: 706141
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 192 amino acids
? TYPE: amino acid
? STRADEDNESS: single
? TOPOLOGY: linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 13:
? -S-10-101-482-13

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Query Match	11.1%;	Score 120;	DB 14;	Length 192;
Similarity	25.3%;	Pred. No. 0.00057;		
Best Local	55;	Conservative	29;	Mismatches 62;
				Gaps 11;

QY 10 TMDPLREETLLADYLGCAREBG--TPEPA-PTSTPEAAVLSSAARLRQIHRSFFSA 66  
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DB 14 TSSEQIMKRGALLGSGFIODRAGRMGGAPALADPVFQDASTKLSECTKIGDEBDS- 72

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QY      67 YLGIFGNRFELVALMADSVLSDSPG-----TWGRVTVLTVAAGTLERG 111
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Db      73 -----NMELQRMIA-AVDVDSPREVFRAVADMSDGNFNWGRVALFYFASKLVKA 124

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QY      112 -----PLVTRARKKKKGFGQPRLKEGEDVARQCRQLVALLSSLTMGQRHAWLQAQGGWDF 166
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Db      125 LCTKPELIRITMGW-----TUDFLREHLG-----WIDQGGWDEL 161

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Qy 167 CHFFRTPEPLAMRKQVQAFSLCULTTAIFYLWRL 203
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Db 162 LSYFGTP---TW-QTWTIVAGVL-TASLTIMKKM 191

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RESULT 9  
US-10-277-693A-9  
; Sequence 9, Application US/10277693A

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; GENERAL INFORMATION:
; APPLICANT: Korschmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Agonists
; Filing Date: 05/06/2008

```

```

; CURRENT APPLICATION NUMBER: US/10/277,693A
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/379,820
; PRIOR FILING DATE: 2000-08-24

```

; PRIOR APPLICATION NUMBER: 08/112,208  
 ; PRIOR FILING DATE: 1993-08-26  
 ; PRIOR APPLICATION NUMBER: 08/856,034  
 ; PRIOR FILING DATE: 1997-05-14

```

; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn version 3.
; SEQ ID NO 9
; LENGTH: 192

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-277-693A-9

```

Query Match	11.1%;	Score 120;	DB 14;	Length 192;
Best Local Similarity	25.3%;	Pred. No. 0.00057;		
Matches 55; Conservative	29;	Mismatches 71;	Indels 62;	Gaps 11

QY 10 TMADPLRERTELLADYLGYCAREPG--TPPEA-PSTPEAAVLRSAAARLRQIHRSFFSA 66  
 14 TSSEQIMKTGALLIGFTIQDRAGRMGGEAPELADVPVQDASTKLSCECLKRIGDELD- 72  
 Db

```

Qy 67 YLGGPNRRBYVALMADSLSDSPCP-----TWRRVYLYVTFACTLLERG 111
      ||:::||::||| ||||| ||::||
Db 73 -----NNELQRMIA-AVDITDSPREVEFRVYAADNFSDGNFMNRGVALLFTFASKVLKA 124
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 112 -----PLVYARMKWKMGFQPLRKEGGVDYARDCQRLVALLSRLMGQBRAMVLAQGSGDGF 166
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 125 LCTKVPBELIRTTIMGW-----TLDFLRRLIG-----WLDQGGMDGL 161
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 167 CHEFRTPPEPLAFWRKOLVOAFPLSCLLTFAFIYIMTRL 203
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 162 LSIFFGTP---TW-QTYTIFVAGVL-TASLTIMKKM 191

```

RESULT 10  
US-10-306-878-5

```

; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; ADDRESS: One Bid

```

; TITLE OF INVENTION: Apoptosis  
 ; FILE REFERENCE: P-LJ 5535  
 ; CURRENT APPLICATION NUMBER: US/10/306.878

;; PRIOR APPLICATION NUMBER: US 60/334,149  
; PRIOR FILING DATE: 2001-11-28  
: NUMBER OF SEQ ID NOS: 28

```

; SEQ ID NO 5
; LENGTH: 192
; TYPE: prt

```

US-10-306-878-5

Query Match

QY	10	TMADPLRETELLADYCYCAREPG--TPEDP-BSTPEAVLRSAARLRQIHRSFPA	66
Malcher	55	Conservative	23
		Malcher	11
		Indels	02
		Gap	24

67 YIGYPGNRFELVALMADSVLSDPGP-----TWGRVTVTFAGTLLERG 11

QY 112 -----PLVTARWKKMGFOPRLKEQEGDVARDQCRLVALLSSRLMGQHRANLQAOGGNDGF 166

167 CHEFRTPEPLAFNRKOLVOAFLSCLLTTFAPLYIMTRL 203

**RESUME 11**

; Sequence 10, Application US/10421285  
 ; Publication No. US20040053836A1  
 ; GENERAL INFORMATION:

```

; APPLICANT: Banerjee, Debabrata
; APPLICANT: Bertino, Joseph R.
; TITLE OF INVENTION: Method for Modulating the Production of a Selected Protein In

```

; CURRENT FILING DATE: 2003-04-22  
 ; PRIOR APPLICATION NUMBER: US 60/375,250  
 ; PRIOR FILING DATE: 2002-04-22  
 ; NUMBER OF SEQ ID NOS: 15

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 192
; TYPE: PRT
; ORGANISM: human
US-10-421-285-10

```

Query Match	11.1%;	Score 120;	DB 15;	Length 192;
Best Local Similarity	25.3%;	Pred. No. 0.00057;		
Matches 55;	Conservative 29;	Mismatches 71;	Indels 62;	Gaps 11.

```

QY      10  TMAADPRERRELLADLYLYCAREEP--TPPEA--STSEAAVLRSSAARLQIHRSPFSA. 66
      11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      14  TSEQIMTKGALLLOSFIODRAGRGMGEAPELADPVQDASTKLSCLRIIGDELD-- 72
      15  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      67  YLIGPGRNFELVALMADSVLSDSPG-----TWGRVVLVTFAAGTLERG 111
      68  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      73  -----NMELQRMIA-AVDTDSPREVPFRVAADMFDGNGFRMGKRVVALPFFASKLVLKA 124
      74  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      112  ----PLVTARWKMGFOPRLKBQSGVDARDCQRLVALLSSRLMGCHRAWLOAQGGMDGF 166
      113  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      125  LCTKVVELIRTIINGW-----TLDFLERELLG-----WIDOGSGWDGL 161
      126  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      167  CHEFRTPPELAFWRKQLOAPLSCLLTFTAIFYLWTRL 203
      168  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      162  LSYFGTP---TW--QVTILFVAGVL-TASLILWKKM 191
      163  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 12
US-09-033-525-2
; Sequence 2, Application US/09033525
; Patent No. US20020090374A1
; GENERAL INFORMATION:
; APPLICANT: Yarkoni, Shai
; APPLICANT: Ben-Yehudah, Ami
; APPLICANT: Azar, Yehudit
; APPLICANT: Agellan, Rami
; APPLICANT: Belotseretsky, Ruth
; APPLICANT: Lorbortoum-Galaki, Haya
; TITLE OF INVENTION: CHEMIC PROTEINS WITH CELL-TARGETING
; TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES
; FILE REFERENCE: 9457-009-999
; CURRENT APPLICATION NUMBER: US/09/033,525
; CURRENT FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
; OS-09-033-525-2

```

Query Match	11.1%;	Score 120;	DB 9;	Length 331;
Best Local Similarity	25.3%;	Pred. No. 0.0011;		
Matches 55;	Conservative 29;	Mismatches 71;	Indels 62;	Gaps 11.

```
QY    10  TMADPARETTELLLDVLYGCARREG--TPEDA-PTSEAVALRSAAARLQIHRSFSA   66
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    153  TSSEQMKTGALLLGFIODRRAGMGGAPEALDVPQDASTKXSECLRIIDEIDS-   211
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    67  YLGYPGNREELVALMDSVLSDSPG-----TWGRVYLVTFAETLLERG   111
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    212  -----NMELQRMIA-AVDTSPREVFPRVAADMFSQGNFRNGRVALLFFPAKLVIKA   263
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    112  ----PLVTARMKKWGFOPRLKEQEGDVARDCCRLVALLSHLWGQHRAWILOAGSGWDGF   166
      -:-|:-|:-|:-|:-|:-|:-|:-|:-|:-|:-|:-|:-|:-|:-|:-|:-|
Db    264  LCTVELIRITINGW-----TLDFLERILIG----WIQDGMDGL   300
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    167  CHEFRTPPLAFWRKDVOAFLSCLLTAFYILWTRL   203
      ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    301  LSYPEGR---TW-QTVITIPVAGVL-TASLIWKKM   330
      ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

```

RESULT 13
US-10-640-668-2
; Sequence 2, Application US/10640668
; Publication No. US20050079154A1
; GENERAL INFORMATION:
; APPLICANT: Yarkoni, Shai
; APPLICANT: Ben-Yehudai, Ahmi
; APPLICANT: Azar, Yehudith
; APPLICANT: Ageilian, Rami
; APPLICANT: Belotserotsky, Ruth
; APPLICANT: Loterbovoun-Galski, Haya
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH
; TITLE OF INVENTION: SPECIFICITY AND APOD
; FILE REFERENCE: 9457-009-899
; CURRENT APPLICATION NUMBER: US/10/640,668
; CURRENT FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: US/09/033,525
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq For Windows Version 3.0.
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-640-668-2

```

Query Match	11.1%;	Score 120;	DB 17;	Length 331;
Best Local Similarity	25.3%;	Pred. No. 0.0011;		
Matches 55;	Conservative 29;	Mismatches 71;	Indels 62;	Gaps 11

[illegible]

```

RESULT 14
US-09-912-599-14
: Sequence 14, Application US/09912599
: Patent No. US20020106731A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Bcl-2-like Polynucleotides, Polypeptides, and Antibodies
: FILE REFERENCE: PTO44P1
: CURRENT APPLICATION NUMBER: US/09/912, 599
: PRIOR FILING DATE: 2001-07-26
: PRIOR APPLICATION NUMBER: PCT/US01/03080
: PRIOR FILING DATE: 2000-01-31
: PRIOR APPLICATION NUMBER: 60/1179,487
: PRIOR FILING DATE: 2000-02-01
: PRIOR APPLICATION NUMBER: 60/180,697
: PRIOR FILING DATE: 2000-02-07
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 23
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-912-599-14

```

Query Match	10.9%;	Score 118;	DB 9;	Length 23;
Best Local Similarity	100.0%;	Pred. No. 6.6e-05;		

	Matches	23;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
OY	181	KQLVQAFISCLTTAFTYLWTRL	203							
Db	1	KQLVQAFISCLTTAFTYLWTRL	23							

```

RESULT 15
US-10-277-693A-2
Sequence 2, Application US/10277693A
Publication No. US20030096367A1
GENERAL INFORMATION:
APPLICANT: Kosemeyer, Stanley J.
TITLE OF INVENTION: Cell Death Agonists
FILE REFERENCE: 56029/36280
CURRENT APPLICATION NUMBER: US/10/277,693A
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 09/379, 820
PRIOR FILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: 08/112, 208
PRIOR FILING DATE: 1993-08-26
PRIOR APPLICATION NUMBER: 08/856, 034
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 2
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-277-693A-2

```

[illegible]

Search completed: June 6, 2005, 10:46:10  
Job time : 54 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2005, 10:37:59 ; Search time 39 Seconds

503.288 million cell updates/sec

Title: US-10-071-174A-2

Sequence: 1 MVDQLRERTTMADPLRERTE.....QAFLSCLTTAFIYLWTRL 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000000

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Listing first 45 summaries

Database : PIR\_79:\*

$$2: \quad \bar{p} \dot{r}_2: *$$

4: pir4:\*

Pred. No. is the num

and is derived by ar

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	193.5	17.9	177	2	S54778	NK-13 protein - qu
2	123	11.3	192	2	D47538	bcl-2-associated f
3	120	11.1	192	2	A47538	bcl-2-associated f
4	113	10.4	143	2	I38921	bcl-2-associated f
5	109	10.1	239	1	TVH0A1	transforming prote
6	108	10.0	350	2	A47476	BCL2 homolog MCL1
7	105.5	9.7	133	2	I53295	bcl-2-associated F
8	101.5	9.4	172	2	I49449	hemopoietic-speci
9	101.5	9.4	236	2	JC7383	B-cell Lymphoma 2
10	101.5	9.4	236	2	I67342	BCL-2 - rat (Iragu
11	100.5	9.3	233	2	A37332	transforming prote
12	99.5	9.2	233	2	B47537	apoptosis regulat
13	99.5	9.2	233	2	I49056	apoptosis regulat
14	99.5	9.2	233	2	SS1761	bcl-x long - mouse
15	99.5	9.2	236	2	I53744	BCL-X protein - rat
16	98.5	9.1	214	2	I49057	gene bcl-2 protei
17	98	9.0	227	2	JR0203	bcl-x transmembran
18	95.5	8.8	205	1	TVH0B1	apoptosis regulat
19	95.5	8.8	255	1	JC7367	transforming prote
20	95	8.8	236	1	TVMSA1	Mcl-1a protein - z
21	94.5	8.7	233	2	I67431	transforming prote
22	94	8.7	232	2	S24390	BCL-X-Long - rat
23	91	8.4	199	1	TVMSB1	transforming prote
24	85.5	7.9	380	2	A75500	aminopeptidase - D
25	84.5	7.8	192	2	A10268	anthranilate synth
26	84	7.7	216	2	B37332	transforming prote
27	83	7.7	272	2	T35231	hypothetical prote
28	82.5	7.6	190	2	I46359	hypothetical prote
29	82	7.6	168	2	A47537	apoptosis regulat

## ALIGNMENTS

30	82	7.6	334	2	T17213	hypothetical prote
31	81.5	7.5	175	2	T139055	Bcl-2 related - hu
32	81	7.5	915	2	T039575	Smoothenin - hum
33	80.5	7.4	179	2	JC7255	Bax-deletin protein
34	80	7.4	209	2	E832241	preprotein transla
35	79.5	7.3	522	1	S01927	nif-specific regul
36	78.5	7.2	200	1	NMBB2D	anthranilate synth
37	78	7.2	218	2	B47538	bcl-2-associated p
38	78	7.2	515	2	T375579	hypothetical prote
39	78	7.2	535	2	T37508	hypothetical prote
40	78	7.2	1632	2	C70752	probable crip1 pro
41	77	7.1	365	2	T34759	oligopeptide ABC t
42	77	7.1	462	2	H70593	hypothetical prote
43	77	7.1	543	2	T34681	probable secreted
44	76.5	7.1	354	2	E87635	efflux system prot
45	76.5	7.1	386	2	T36169	hypothetical prote

## RESULT 1

NR-13 protein - quail  
C/Species: *Coturnix coturnix* (quail)  
C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jul-2000  
C/Accession: S54778  
R/Gillet, G.; Guerin, M.; Trembleau, A.; Brun, G.  
EMBO J. 14, 1372-1381, 1995  
A/Title: A BCL-2-related gene is activated in avian cells transformed by the Rous sarcoma virus  
/Reference number: S54778; MUID:95246730; PMID:7729415

A;Cross-references: EMBL:X84418; NID:g790983; PIDN:CAA59136.1; PID:g790984

	Query Match	17.9%	Score 193.5	DB 2	Length 177;	
	Best Local Similarity	33.1%	Pred. No. 2.4e-11;			
	Matches	57;	Conservative 16;	Mismatches 56;	Indels 43;	Gaps 6
Qy	11	MADPLRERTELLADYLGYCAREPCTPPAPSPAPEAAVLRSAARLRIQHRSFPAVL--	68			
Db	1	MPSTLKEETALLLEDYFGH--RAGGALPPSAT--AAELRRMAALELERRERPFRSCAPL	56			
Qy	69	--GYPNRRRELYALMADSVLSDSPCPPTGRVVTLYTFNGTL-----LERGLVTARKW	118			
Db	57	ARAARPPEAALRLRKVAQALETLDG--GIINGRILLTALVFEGTIAALAASACBEP-----	109			
Qy	119	KKAQFPRLKEGGVDVARQCQLVALLSRLMGCHRALIQGGMDGCFHF	170			
Db	110	-----SRLTAALTAVYLAIRGGEMWEHHGGDGCRCFF	141			

## RESULT 2

bcl-2-associated protein x - mouse  
N:Alternate names: BAX; programmed cell death membrane protein x  
C:Species: Mus musculus (house mouse)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 28-Jul-2003  
C:Accession: D47538  
R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.  
Cell 74, 609-619, 1993  
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates p  
A:Reference number: A47538; MUID:93364978; PMID:8358790  
A:Accession: D47538  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-192 <OLT>  
A:Cross-references: GB:L22472  
C:Genetics:  
A:Gene: bax  
A:Superfamily: bcl apoptosis regulator, inhibitory type



R.Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.  
Oncogene Res. 2, 263-275, 1988  
A>Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:  
A:Reference number: A27622; MUID:88217344; PMID:3285301  
A:Accession: A27622  
A:Molecule type: mRNA  
A:Residues: 1-58, 'T', 60-239 <HUA>  
A:Accession: B27622  
A:Molecule type: DNA  
A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA2>  
A>Note: the sequence was determined from the germine gene  
C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation  
C:Genetics:  
A:Gene: GDB:BCL2  
A:Cross-references: GDB:119031; OMIM:151430  
A:Map position: 18q21.3-18q21.3  
C:Function:  
A:Description: blocks apoptosis in hematopoietic cells  
C:Superfamily: bcl apoptosis regulator, inhibitory type  
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 10.1%; Score 109; DB 1; Length 239;  
Best Local Similarity 23.5%; Pred. No. 0.0052;  
Matches 52; Conservative 20; Mismatches 65; Indels 84; Gaps 11;

Qy 28 GYCARPG-TPEPA-----PSTPEA-----VLRSA----- 52  
Db 47 GIPSSQPHTHPAASRDPAVTSPLQTPAAGALSVPPVHLLTLOAQDDBSR 106  
Qy 53 -----AARLRQIHRSPFSAVLYGPGNRFELVALMADSVLSDPGPTWGRVTLTVPAGT 106  
Db 107 RYRDPFAMSSQLHTLPFTA-----RGRF---ATVEELFRD--GVNNGRIYAFPEFGV 156  
Qy 107 LL-----ERGPLVTARMKKMGFQPRLEQSGDVARDCCRLVALSSRLMGH-RAWIOA 159  
Db 157 MCVSVNEMSPLYDN-----IALMWTETYNHHLHTWIOD 191  
Qy 160 QGMDGFCHEFRTPF-PLAFWRKOLVOAFLSCLLTAPFIYL 199  
Db 192 NGMDAFVELYGPSMRPLPFPSSWLSLKTLLSLALVACITLL 232

## RESULT 6

A47476  
BCL2 homolog MCL1 - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Feb-1997  
C:Accession: A47476  
R:Kozopas, K.M.; Yang, T.; Buchan, H.L.; Zhou, P.; Craig, R.W.  
Proc. Natl. Acad. Sci. U.S.A. 90, 3516-3520, 1993  
A>Title: MCL1, a gene expressed in programmed myeloid cell differentiation, has sequence  
A:Reference number: A47476; MUID:93234528; PMID:7682708  
A:Accession: A47476  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-350 <KOZ>  
A:Experimental source: ML-1 myeloid cell leukemia  
A>Note: sequence extracted from NCBI Backbone (NCBI:129734)  
C:Keywords: transmembrane protein

Query Match 10.0%; Score 108; DB 2; Length 350;  
Best Local Similarity 23.8%; Pred. No. 0.01;  
Matches 49; Conservative 20; Mismatches 71; Indels 66; Gaps 8;

Qy 13 DPLRETELL-LADYLGACAREPGTPPEAPSTP----- 44  
Db 132 EPLGRPAVLPLLELVGSSGNNSTSDGSLPSTPPAESEBDELVQSLIISRYLREQAT 191  
Qy 45 -----EAYVRSAAARLRQI-----HNSFSAVLYGPG--NRFELVALMADSV 85  
Db 192 GAKDTKPMGRSGATSRKLETLLRRVGDVQRNHEVTFQGLRKLDIKNEDVKSLSRYMI 251  
Qy 86 LSDSPGPT-WGRVVTLVTFAGTLERGLVTAARWKMGFQPRLEQSGDVARDCCRLVAL 144

Db 252 HVFSDGVTNMGRIYTLISF-----GAFVAKHLK-----TINQESCI-----EPLAES 293  
Qy 145 LSSRLMGHRAMLOAQSGMDGFCHEF 170  
Db 294 ITDVLVRRTRDMLVQRGMDFVEFF 319

## RESULT 7

153295  
bcl-2-associated protein x - rat (fragment)  
N:Alternate names: BAX; programmed cell death membrane protein x  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: 153295  
R:Rilly, J.L.; Rilly, K.L.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 233-241, 1995  
A>Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin  
onstitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.  
A:Reference number: 153295; MUID:95129487; PMID:7828536  
A:Accession: 153295  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-133 <RES>  
A:Cross-references: UNIPROT:Q63690; EMBL:U32098; NID:9975869; PIDD:AAA75200.1; PID:99758

Query Match 9.7%; Score 105.5; DB 2; Length 133;  
Best Local Similarity 27.2%; Pred. No. 0.0058;  
Matches 44; Conservative 16; Mismatches 43; Indels 59; Gaps 9;

Qy 36 TPE-PAEPPEAAVIRSAARLRQIHRSPFSAVLYGPGNRFELVALMADSVLSDPGP-- 92  
Db 6 TPELTLEQPPQDASTKSLSECLRIIDEL-----DNNMELQRMID-VDTSPREVF 56  
Qy 93 -----TWGRVYTLVTFAGTLERGLVTAARWKMGFQPRLEQSGDVARDCC 139  
Db 57 FRVAADMFADGNFMGRVVALFYPSKLV-----IKAL-----CT 91  
Qy 140 RLVALSSRLMG-----QHR--AWLOAQSGMDGFCHEFRTP 173  
Db 92 KVPBLIRT-IMGWTLDFRLERLFWIODQSGMDGLSTFGTP 132

## RESULT 8

149449  
hemopoietic-specific early-response protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: 149449  
R:Lin, E.Y.; Orloffsky, A.; Berger, M.S.; Prytcowsky, M.B.  
J. Immunol. 151, 1979-1988, 1993  
A>Title: Characterization of A1, a novel hemopoietic-specific early-response gene with a  
A:Reference number: 149449; MUID:93346743; PMID:8345131  
A:Accession: 149449  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-172 <RES>  
A:Cross-references: UNIPROT:Q07440; GB:U16462; NID:9293273; PIDD:AAA16886.1; PID:9293274

Query Match 9.4%; Score 101.5; DB 2; Length 172;  
Best Local Similarity 23.6%; Pred. No. 0.019;  
Matches 39; Conservative 31; Mismatches 66; Indels 29; Gaps 8;

Qy 22 LLDYLGACAREPGTPPEAPSTPEAAVIRSAARLRQIHRSPFSAVLYGPGNRFELVALM 81  
Db 12 LAEHYLOVTLQVAP-ESAPSOACRVLOVAFSVQKEVEKLSYLDPFVESITDKRIT 70  
Qy 82 ADVSLS--DSPGPTWGRVVTLVTFAGTLERGLVTAARWKMGFQPRLEQSGDVARD- 137  
Db 71 FNQVMEKFEEDGIINMGRIYTLIFAFGVLLKLP-----QEO---IALDV 112



C:Keywords: alternative splicing; apoptosis  
F:1-233/Product: apoptosis regulator bcl-xl #status predicted <MA1>  
F:1-125,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>

Query Match  
Best Local Similarity 23.1%; Pred. No. 0.042;  
Matches 31; Conservative 19; Mismatches 57; Indels 27; Gaps 4;

Qy 44 PEAAY--LRSAARLRQIHRSFSAVIGY---PGNRFELVALMADSVLSDSPGPTWGR 96  
Db 82 PMAAVKQALREAGDFELRYRRAFSDLTSQHLITPTGTAYQSFQGVNLEFRD--GVNNGR 139  
Qy 97 VVTLVTFAGTLLERGPLVTARKWKGFQPRLEKQSGDVARDCCQRLVALLSRL---MGQH 156  
Db 140 IVAFPSFGALC-----VESVKEMQVLSRIASMMATYTLNDH 181  
Qy 157 LQAQGGMDGFCGFF 170  
Db 182 IQENGMDTFVLDY 195

## RESULT 13

149056  
bcl-x long - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: 149056; S52866  
R:Yang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.M.  
J. Immunol. 153, 4388-4398, 1994  
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A:Reference number: 149055; MUID:95052604; PMID:7963517  
A:Accession: 149056  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-233 <RES>  
A:Molecule type: mRNA  
A:Cross-references: UNIPROT:064373; EMBL:U10101; NID:g506647; PID:AA82173.1; PID:g5066  
R:Kamezaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.  
submitted to the EMBL Data Library, November 1994  
A:Description: IL-5 inhibits anti-1gM-induced apoptosis in an immature B cell line throu  
A:Reference number: S52866  
A:Accession: S52866  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-233 <KAM>  
A:Cross-references: EMBL:X83574; NID:g695622; PID:CAA58557.1; PID:g695623  
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match  
Best Local Similarity 24.6%; Pred. No. 0.042;  
Matches 34; Conservative 17; Mismatches 52; Indels 35; Gaps 6;

Qy 44 PEAAY--LRSAARLRQIHRSFSAVIGY---PGNRFELVALMADSVLSDSPGPTWGR 96  
Db 82 PMAAVKQALREAGDFELRYRRAFSDLTSQHLITPTGTAYQSFQGVNLEFRD--GVNNGR 139  
Qy 97 VVTLVTFAGTLLERGPLVTARKWKGFQPRLEKQSGDVARDCCQRLVALLSRL---MGQH 153  
Db 140 IVAFPSFGALC-----SVDKEMQVLSRIASMMATYTLNDH 177  
Qy 154 -RAWLQAQGGMDGFCGFF 170  
Db 178 LEPWIQENGMDTFVLDY 195

## RESULT 14

551761  
Bcl-X protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C:Accession: S51761; S51762  
R:Michaelidis, T.M.  
submitted to the EMBL Data Library, November 1994  
A:Reference number: S51761

A:Accession: S51761  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-233 <MIC>  
A:Cross-references: UNIPROT:P53563; EMBL:X82537; NID:g607176; PID:CAA57886.1; PID:g6071  
A:Experimental source: embryonic; brain  
A:Accession: S51762  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-125,189-233 <MI2>  
A:Cross-references: EMBL:X82537; NID:g607176; PID:CAA57887.1; PID:g607178  
A:Experimental source: embryonic; brain  
A>Note: smaller form due to splicing  
C:Genetics:  
A:Intron: 125/3  
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match  
Best Local Similarity 24.6%; Pred. No. 0.042;  
Matches 34; Conservative 17; Mismatches 52; Indels 35; Gaps 6;

Qy 44 PEAAY--LRSAARLRQIHRSFSAVIGY---PGNRFELVALMADSVLSDSPGPTWGR 96  
Db 82 PMAAVKQALREAGDFELRYRRAFSDLTSQHLITPTGTAYQSFQGVNLEFRD--GVNNGR 139  
Qy 97 VVTLVTFAGTLLERGPLVTARKWKGFQPRLEKQSGDVARDCCQRLVALLSRL---MGQH 153  
Db 140 IVAFPSFGALC-----SVDKEMQVLSRIASMMATYTLNDH 177  
Qy 154 -RAWLQAQGGMDGFCGFF 170  
Db 178 LEPWIQENGMDTFVLDY 195

## RESULT 15

153744  
gene bcl-2 protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C:Accession: 153744  
R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.  
Gene 140, 291-292, 1994  
A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.  
A:Reference number: 153744; MUID:94193015; PMID:8144041  
A:Accession: 153744  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <RES>  
A:Cross-references: UNIPROT:P49950; GB:L14680; NID:g408946; PID:AA53662.1; PID:g408947  
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match  
Best Local Similarity 25.8%; Pred. No. 0.043;  
Matches 40; Conservative 17; Mismatches 61; Indels 37; Gaps 7;

Qy 50 RSAARLRQIHRSFSAVIGY---PGNRFELVALMADSVLSDSPGPTWGRVTLVTFAGTLL 109  
Db 107 RDEAFMSQHLTPPTA-----RGRF--ATVEELFRD--GVNNGRIAVAFEEFGVNC- 155  
Qy 110 RGPLVTARKWKGFQPRLEKQSGDVARDCCQRLVALLSRL---MGQH 165  
Db 156 -----VGSVNRMSPLVDNIALMTETVLRHLHTWIQDNGMDA 194

Qy 166 FCHFRTPF-PLAFWRKQVQAFSLCTTFAIYL 199  
Db 195 FVELYGPGRPLFDRPSLSTKLTLALVGCITL 229

Search completed: June 6, 2005, 10:44:23  
Job time : 40 secs

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2005, 06:21:30 ; Search time 282.584 Seconds  
(without alignment)  
5136.091 Million cell updates/sec

Title: US-10-071-174A-1

Perfect score: 887  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:\*

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- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55.6	6.3	2508	US-09-949-016-1466	Sequence 1466, Ap
2	55.6	6.3	97989	US-09-949-016-13208	Sequence 13208, A
3	55.2	6.2	5808	US-09-902-540-794	Sequence 794, App
4	54.8	6.2	6599	US-09-902-540-879	Sequence 879, App
5	54.4	6.1	1614	US-09-902-540-8389	Sequence 8389, Ap
6	54.4	6.1	7186	US-09-902-540-879	Sequence 879, App
7	52.8	6.0	1467	US-09-902-540-8509	Sequence 8509, Ap
8	52.8	6.0	6482	US-09-902-540-896	Sequence 896, App
9	52	5.9	3198	US-09-902-540-2522	Sequence 2522, Ap
10	52	5.9	17503	US-09-902-540-1114	Sequence 1114, Ap
11	51.4	5.8	967	US-09-902-540-7886	Sequence 7886, Ap
12	50.2	5.7	888	US-09-902-540-9238	Sequence 9238, Ap
13	50.2	5.7	2199	US-09-902-540-6388	Sequence 6388, Ap
14	50.2	5.7	2585	US-09-902-540-424	Sequence 424, App
15	50.2	5.7	9818	US-09-902-540-987	Sequence 987, App
16	49.8	5.6	1194	US-09-724-797-25	Sequence 25, Appl
17	49	5.5	678	US-09-902-540-4171	Sequence 4171, Ap
18	49	5.5	22301	US-09-902-540-1208	Sequence 1208, Ap
19	48.6	5.5	1702	US-09-902-540-8057	Sequence 8057, Ap
20	48.6	5.5	7160	US-09-902-540-821	Sequence 821, App
21	48.4	5.5	1092	US-09-252-991A-8481	Sequence 8481, Ap
22	48.4	5.5	3678	US-09-252-991A-8447	Sequence 8447, Ap
23	48	5.4	2561	US-09-616-289-48	Sequence 48, Appl
24	47.8	5.4	1362	US-09-724-797-31	Sequence 31, Appl
25	47.8	5.4	1365	US-09-252-991A-9680	Sequence 9680, Ap
26	47.8	5.4	1395	US-09-252-991A-9641	Sequence 9641, Ap
27	47.8	5.4	1443	US-09-252-991A-9615	Sequence 9615, Ap

28	47.6	5.4	2028	US-09-902-540-7619	Sequence 7619, Ap
29	47.6	5.4	7850	US-09-902-540-749	Sequence 749, App
30	47.4	5.3	1382	US-09-016-434-1256	Sequence 1256, Ap
31	47.4	5.3	1707	US-09-252-991A-10297	Sequence 10297, A
32	47.4	5.3	2511	US-09-252-991A-10560	Sequence 10560, A
33	47	5.3	1428	US-09-252-991A-14802	Sequence 14802, A
34	47	5.3	1668	US-09-252-991A-14950	Sequence 14950, A
35	46.8	5.3	711	US-09-902-540-9612	Sequence 9612, Ap
36	46.8	5.3	1380	US-09-902-540-5345	Sequence 5345, Ap
37	46.8	5.3	1393	US-09-902-540-9055	Sequence 9055, Ap
38	46.8	5.3	1633	US-09-902-540-6509	Sequence 6509, Ap
39	46.8	5.3	2605	US-09-902-540-470	Sequence 470, App
40	46.8	5.3	13299	US-09-902-540-968	Sequence 968, App
41	46.8	5.3	13631	US-09-902-540-1092	Sequence 1092, Ap
42	46.8	5.3	34662	US-09-902-540-1261	Sequence 1261, Ap
43	46.6	5.3	2403	US-09-949-016-1543	Sequence 1543, Ap
44	46.6	5.3	3252	US-10-327-189-3	Sequence 3, Appl
45	46.4	5.2	1344	US-09-252-991A-11619	Sequence 11619, A

## ALIGNMENTS

```

RESULT 1
US-09-949-016-1466
; Sequence 1466, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1466
; LENGTH: 2508
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1466

Query Match      6.3%  Score 55.6;  DB 4;  Length 2508;
Best Local Similarity 46.2%;  Pred. No. 0.00036;
Matches 257;  Conservative 0;  Mismatches 294;  Indels 5;  Gaps 2;

QY      15 CAGCGAAGCCCGCCCGCCAGAGGCGGACCATGTTGACCACTTGGCGGACGCA 74
DB      1624 CGGCGACCCCGCCCGCCCGCCCGCCAGAGGCGGACCATGTTGCGAGCGAG 1683
QY      75 CCACCATGCGCGACCCCGCGCGGAGCGCACCGACTTCTGGCCGACCTACTGGGGT 134
DB      1684 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1743
QY      135 ACTGCGCCCGCGGAAACCGCGGACCCCGGAGCGGCGCATCATCGCGCGGAGCGCGTG 193
DB      1744 ACTGCGCCCGCGGAAACCGCGGACCCCGGAGCGGCGCATCATCGCGCGGAGCG 1803
QY      194 CTGCGCTCCCGCGCGCGCGCGGATTCAGCGAGTTACCGGCTCTTCTCCGCTTACTC 253
DB      1804 GTGCGCTCCCGCGCGCGCGCGGATTCAGCGAGTTACCGGCTCTTCTCCGCTTACTC 1863
QY      254 GCGTACCCCGGAAACCGGTTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 313
DB      1864 AG----CCCGGAAACCCCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1919
QY      314 AGCCCGGCGCCACCTCGGCGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 373

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Db 1920 TGACCTTCCCAACACCGGGCCAGCAACCAACAGCCCGGAGGCTCCAGGCTCTGGAGCTG 1979  
QY 374 GAGAGAGGCGCGCTGTATACCGCCCGGTGAAGAGTGGGGCTTCCACCCGCGCTAAG 433  
Db 1980 CAGAGAGGAGAACTGAGCACTACCGGATGGAGATGAACCTTGTCTGATGATGAGACG 2039  
QY 434 GAGCAGAGAGGCGAGCTGCGCCCGGAGCTGCCAGCGCTGTGGCTTGTGAGCTTCGCGG 493  
Db 2040 CATCCCGAAGAAAGACGTACAGCAAGGCGCGCTGCGCGGAGCTTGGGGAGACACAC 2099  
QY 494 CTGATGGGCGAGCACCGCGCTGTGCTGAGCTCAGGCGCGCTGGAGTGGCTTTTGTAC 553  
Db 2100 CGCCCGAGGACCGGGGCTTGGGGGTGAGAGACTGCGGTCCAGAGCCCAAGAGAG 2159  
QY 554 TTCTTCAGAGACCCCT 569  
Db 2160 AACTTCAGGCGCGCT 2175

## RESULT 2

US-09-949-016-13208  
; Sequence 13208, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH INFECTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13208  
; LENGTH: 97989  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(97989)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13208

Query Match 6.3%; Score 55.6; DB 4; Length 97989;

Best Local Similarity 46.2%; Pred. No. 0.0014;

Matches 257; Conservative 0; Mismatches 294; Indels 5; Gaps 2;

QY 15 CAGCGAAGGCGCGCGCCCGCCAGCAGAGCGGACCATGGTTGACCATGTTGGCGGAGCGCA 74  
Db 89050 CGGCCACCGCGCGCGCGCGCGCGCGCCAGGAAAGGTCGCCCATCTTCTGAGAGAG 89109  
QY 75 CCACCATGGCGGACCGCGCGCGGAGCGGACCGGAGCTGTGTGGCCGACTACCTGGGGT 134  
Db 89110 TGTGCTGTGACAGAGAGCGGGCGGGGACATCAATGTCTCTGAGAGGCGGGCGGGG 89169  
QY 135 ACTGGCGCGGGAACCGCGGACCGCGGAGCGG-CCGATTCACCGCGGAGCGCGCTG 193  
Db 89120 ACTGGCGCGGAGCAGAGCTGGGGCGAGAGCAGCGCGGGGCTCCAGGGGTGTCCGACAG 89229  
QY 194 CTGCGCTCGCGCGCGCGCAGGATTACGCGGATTCACCGGCTCTTTTCTCGCGCTACCTC 253  
Db 89230 GTGCTCTCGCGCGCGCTGCTGTGATGACTTCGCAACCGAGGTTCCGAGCCCAAGC 89289  
QY 254 GGTACCGCGGGAACCGCTTGAAGTGTGAGCGGCTGATGGCGGATTCGGGTCTCTCCAGC 313  
Db 89290 AG---CCCGGGAACCCCAAGCGCGGAGCGGCGGAGTCAACCCCGGTGTTACG 89345

QY 314 AGCCCGGCGCCCACTGCGGAGAGTGTGACGCTGTGACCTTTCGAGGAGCGCTGTG 373  
Db 89346 TGACCTTCCCAACACCGGGCCAGGAAACAGCCCGGAGGCTCCAGGCTCTGGAAGCTG 89405  
QY 374 GAGAGAGGCGCGCTGTATACCGCCCGGTGAAGAGTGGGGCTTCCAGCCCGCTAAG 433  
Db 89406 CAGAGAGGAGAACTGAGCACTACCGGATGGAGATGAACCTTGTCTGATGATGAGACG 89465  
QY 434 GAGCAGAGAGGCGAGCTGCGCCCGGAGCTGCCAGCGCTGTGGCTTGTGAGCTTCGCGG 493  
Db 89466 CATCCCGAAGAAAGACGTACAGCAAGGCGCGCTGCGCGGAGCTTGGGGAGACACAC 89525  
QY 494 CTGATGGGCGAGCACCGCGCTGTGCTGAGCTCAGGCGCGCTGGAGTGGCTTTTGTAC 553  
Db 89526 CGCCCGAGGACCGGGGCTTGGGGGTGAGAGACTGCGGTCCAGGCGCCCAAGAGAG 89585  
QY 554 TTCTTCAGAGACCCCT 569  
Db 89586 AACTTCAGGCGCGCT 89601

## RESULT 3

US-09-902-540-794  
; Sequence 794, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(115849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 794  
; LENGTH: 5808  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-794

Query Match 6.2%; Score 55.2; DB 4; Length 5808;

Best Local Similarity 47.6%; Pred. No. 0.0061;

Matches 162; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 52 GATTGACCAATTGGGAGGCGCACCAATGCGGACCCGCTGCGGAGCGCACCGAGCT 111  
Db 4805 GTTGACCAATCTCCAGTCCCAAGAAAGTTGGCGGATGGAGCTGGAGCGGCCATGCT 4864  
QY 112 GTTGCGGCGCACTACTGAGGATCTGCGCGCGGGAACCGGCAACCGCGGAGCGCGC 171  
Db 4865 GAGGCGGACACAGACGCGGAGGCTGTGGGGGACCTTGTACAGCGGCGGTCCGC 4924  
QY 172 ATTCAGCGCCGAGGCGCGCGCTGCTGCGCGCGCGCAGGTTACGCGAGATTACCG 231  
Db 4925 CCATCCGCGCGCTGTGCGGGGATGTTGTGCGGAGCGCGCGCGCTGTGCTGCGCGC 4984  
QY 232 GTCTTTTCTCCGCTTACTGCGGCTTCCGCGGAAACGCTTTCAGCTGTGTGGCTGAT 291  
Db 4985 CGCGGCGCTGTGGGCTTGTGAGAGACCCGCGGTGACATACGCGCTGTGTGCTGGG 5044  
QY 292 GCGCGATTCCGTGCTTCCAGCAGGCGCGCGCCCACTGGGAGAGAGTGTGAGCTGTGT 351  
Db 5045 CGCGGTGCTGCGCTGT 5104  
QY 352 GACTTTCAGAGAGCGTGTGTGAGAGAGGCGCGTGTGTG 391  
Db 5105 GGGGT 5144

## RESULT 4

US-09-902-540-724  
; Sequence 724, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(115849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 724  
; LENGTH: 6599  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-724

Query Match 6.2%; Score 54.8; DB 4; Length 6599;  
Best Local Similarity 45.4%; Pred. No. 0.0081;  
Matches 197; Conservative 0; Mismatches 237; Indels 0; Gaps 0;

QY 22 GGGCCGGCCCCCGAGAGGCGGAGCCATGCTTGACAGCTGGCGGGAGCCGACCCAGC 81  
DB 2463 GAACTGCGCCCAAGACCTGTACTCTATCTCCGCTCGACCGGCTGAGTACCCACAC 2522  
QY 82 GGGCGACCCCGCTGCGGGAGCGACCGAGCTGTGCTGGCGCGCACTACCTGAGGTACTGCGC 141  
DB 2523 GCTGTACCCCGACACTGTGTGCGCGCGCTGACGCGCTGAGCCGCTACCTGAGGTACTG 2582  
QY 142 CCGGAGACCCGACACCCCGAGCGCGCCATCCACGCGCGCGCGCTGCTGCGCTC 201  
DB 2583 CTGTGTACGCGCGCTCACTGCTGCTGCGCTGAGATGCGCAACCCGCTTCTCTC 2642  
QY 202 GCGCGCGCGCGAGTTAGCGGAGATTCAACCGGCTTTTCTCCGCTACCTCGGCTACCC 261  
DB 2643 GCGCTAGTGTGGCGCTGCGCGCTGAGCTTCCGATTCCTGCTGCGACCTGAGCGCGC 2702  
QY 262 GGGGACCGCTTTCAGCTGTGTGCGCTGATGCGGAGATTCCGCTCTCCGACAGCCCGG 321  
DB 2703 CACCTGCGCGCGCGCTGCTGCGCTGCGCTTCCGCTTACCGGACACTTCACTGCGGCTT 2762  
QY 322 CCGCACTGCGGAGAGTGTGACGCTGCTGACCTTTCGAGGAGCGCTGCGAGAGG 381  
DB 2763 CATCAACTAGCGCGCGCTGCGCTGACGCTGCTGCTGCGGCTCTTCTGTCGGAGC 2822  
QY 382 GCGCGTGTGACCGCGCGCTGAGAGAACTGGGGCTTTCAGCGCGCGCTTAAAGAGACAGA 441  
DB 2823 GCTGAGAGACACGCGCTGCGCGCGAGCGTGGGGCTGCGGCTGCGGCTGCTGCTGCTG 2882  
QY 442 GGGCGACGTCGCC 455  
DB 2883 GGTGCTCTCTTCC 2896

RESULT 5  
US-09-902-540-8389  
; Sequence 8389, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(115849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 8389  
; LENGTH: 1614  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-8389

Query Match 6.1%; Score 54.4; DB 4; Length 1614;  
Best Local Similarity 46.5%; Pred. No. 0.0061;  
Matches 175; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 130 GGGGTACTGCGCCCGGGAACCCGACCCCGAGCGCGCATTCACGCGCGAGCGC 189  
DB 645 GAGTACGTGGCGGAGAGCGAAGGCTGCTGAGGACAGACGTACAGGCTGAGGCTTAC 704  
QY 190 CTGTGCTGCTGCGCGCGCGGAGTTACGCAATTCACCGGTCTTTTCTCCGCTA 249  
DB 705 CTTCGCCACCGCTGAGCGCGCGCTGCGCGCGCGCTGCGCGCGCTTCTTACAGGCGTT 764  
QY 250 CCGGCTACCCCGGGAACCGCTTCAAGCTGTGCGCTGATGAGCGATTCGCTCTC 309  
DB 765 GCGCTTACCGGAGCTGCGATGACCTGTGTGAGGCGGCGCAAGGCGCTATGCGG 824  
QY 310 CGAGACCCCGCGCCCACTGCGGAGAGTGTGACGCTGTGACCTTTCGAGGAGCGCT 369  
DB 825 CGAGGACTGGGCGGAGAGCGAGCGTCCGAGTCTGCGCGCTGAGCTTCAAGACGGA 884  
QY 370 CTGTGAGAGAGCGCGCTGTGTGACCGCGCGGTGTGAAGAGTGGGCTTTCAGCGCGCT 429  
DB 885 CTGTGTTCATGATGATGACGCGCGCTTCTGTGTGAGATGAGGACAGCTGTGCGCT 944  
QY 430 AAAGAGAGAGAGGCGGCGGCGCGCGCGGACCTGCGAGCGCTGTGCTTGTGAGCTC 489  
DB 945 GAAAGAGCGATGAGGACCTTATGCGCGCGCGGAGCGCGCGCGGAGAGCGGAGCA 1004  
QY 490 GCGGCTCATGCGGCGAG 505  
DB 1005 CTGTGTATGCGGCTG 1020

RESULT 6  
US-09-902-540-879/c  
; Sequence 879, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(115849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 879  
; LENGTH: 7186  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-879

Query Match 6.1%; Score 54.4; DB 4; Length 7186;  
Best Local Similarity 46.5%; Pred. No. 0.0011;  
Matches 175; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 130 GGGGTACTGCGCCCGGGAACCCGACCCCGAGCGCGCATTCACGCGCGAGCGC 189  
DB 5491 GAGTACGTGGCGGAGAGCGAAGGCTGCTGAGGACAGACTTACGCGCTGAGGCTTAC 5432  
QY 190 CTGTGCTGCTGCGCGCGCGGAGTTACGCAATTCACCGGTCTTTTCTCCGCTA 249  
DB 5431 CTTCGCCACCGCTGAGCGCGCGCTGCGCGCGCTGCGCGCGCTTCTTACAGGCGTT 5372

Qy	250	CCTGGGCTAACCCCGGGAAACCCGCTTCGACGTGTGTGGCGTGAATGGCGGATTGCCGTGCTCTC	309
Db	5371	CGCCCTTCACCGGACGTGCATGACCTGTCTGTGTGGAGCGGCCCAAGGGCGGCATGCGCGG	5312
Qy	310	CGACACGCCCGGCCCCACCTCGTGGGCGAGTGTGTACGCTCTGTGACCTTTGCGAGGGACGCT	369
Db	5311	CGAGGGAATGGGCGCCGAGACGACGATGCGCCGATCTGTGCTGCGCTGAGCTTCACAGACGACGGA	5252
Qy	370	GCTGGAGAGAGGGCCCGCTGTGTGACCGCGCCGGTGTGAAGAATGTGGGCTTTCGACCGCGCGCT	429
Db	5251	CTGGGTGTTCCATGATGATGACGGGCGCTTACTCTGTGGGAGATGTGAGACACGCTGTGTGGCT	5192
Qy	430	AAAGAGACGAGAGGGCGACGTGCGCCCGGAGCTGCGACGCGCTGTGTGGCTTGTCTGAGCTC	489
Db	5191	GGACACAGCGATGTGGGCAACTTCATGCGCGCGGACGAGCGCGCCGCGGGAGGACCGCGGCA	5132
Qy	490	GCGGCTCATGGGGCGAG	505
Db	5131	CTGTGTCAATCGCGCTG	5116

```

RESULT 7
US-09-902-540-8509
; Sequence 8509, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(11849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIORITY FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8509
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8509

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Query Match	6.0%;	Score 52.8;	DB 4;	Length 1467;
Best Local Similarity	48.4%;	Pred. No. 0.0015;		
Matches 147; Conservative	0;	Mismatches 157;	Indels 0;	Gaps 0;

Oy 164 CCGGCGGCATTCACGCGCCGAGGCGCGCGTGGCTTCGCGCGCGCCGACAGTTACGGGACG 223  
 Db 478 CAGGCCCCCGGTATACCGGAGGCGGTGGAGACGGGCGCCATGTGGTGGCATTGGCGCCC 557  
 Oy 224 ATTCAACCGGTCTCTTTTCTCCGCTACTCTGGGCTACCCGGGGAACGGCTTCGAGCTGGTG 283  
 Db 538 TCGCAGGTGCGGCTTCGGCACTTTCGAGTCTTTCATCAACGAGAGACCGGACGTC 597  
 Oy 284 GCGCTGATGCGCGAATTCGCGTCTCTCCGACAGCGCCCGGCGCCCACTTGGGGCAGAATGGTG 343  
 Db 598 GCCAGCGTGGCCGACCACTCATCAACGAGCACTTCCCACTCCGCGGCCAGGAAGGC 657  
 Oy 344 ACGCTGTGACCTTCGACAGGAGCGCTGCGAGAGAGGCGCGTGGTGAACGCGCCGATGG 403  
 Db 658 CGCTACGGCGGCTTTCATCAACGAGGAGTGGTGGAGCGCACGCGCGGCTGATTGGCGCATGG 717  
 Oy 404 AAGAAGTGGGGCTTCAGCGCGCGGCTTAAAGGAGCAGAGAGGCGCAGCTGCGCCGGGACTGG 463  
 Db 718 CAGGCGGTGGGCTTCCGCCACAGGGGTGAATGAACACGGAACAACATGTCTCATCTTGGGCTTC 777  
 Oy 464 CAGC 467  
 Db 778 ACGC 781

```

RESULT 8
US-09-902-540-896
; Sequence 896, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15848)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 896
; LENGTH: 6482
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-896

```

Query Match	6.0%	Score 52.8	DB 4	Length 6482
Best local Similarity	48.4%	Pred. No. 0.0026		
Matches 147	Conservative	0	Mismatches 157	Indels 0
				Gaps 0

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RESULT 9
US-09-902-540-2522
; Sequence 2522, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Miegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(1584)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID.NOS: 16825
; SEQ ID NO 2522
; LENGTH: 3198
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2522

```

Query Match 5.9%; Score 52; DB 4; Length 3198;  
Best Local Similarity 53.4%; Pred. No. 0.0032;  
Matches 109; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

18 CGAAGCCCGGCCCCCGGAGAGCCGACCATGTTGACGTTGGGGAGCGCACCA 77  
Db CGAAGACCATCTCGCTTACAGAGAGCTGGCCAGATTCAATGAGAGCGGCGCTCA 823  
Qy 78 CCATGCGCGGACCCCGCTGGGGAGCGCACCATGTTGCTGGCCCACTACTGGGGTACT 137  
Db 824 CCGAGGCGGAGCTGTCTGACGCGAGATTGAAGTCTGACCCCGAGAGACCCGAGCTGG 883  
Qy 138 GCGCCCGGGAACCGCGGACCCCGGAGCGGCGCATCCACGCGCGGAGCGCGGTGCTGC 197  
Db 884 TCGGCGCGCGCGCGCGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCTCAGC 943  
Qy 198 GCTCCG 221  
Db 944 CCGCCCG 967

RESULT 10  
US-09-902-540-1114/c  
; Sequence 1114, Application US/09902540  
; Patent No. 6833447

GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1114  
; LENGTH: 17503  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-1114

Query Match 5.9%; Score 52; DB 4; Length 17503;  
Best Local Similarity 53.4%; Pred. No. 0.0059;  
Matches 109; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

18 CGAAGCCCGGCCCCCGGAGAGCCGACCATGTTGACGTTGGGGAGCGCACCA 77  
Db 10937 CGAAGACCATCTCGCTTACAGAGAGCTGGCCAGATTCAATGAGAGCGGCGCTCA 10878  
Qy 78 CCATGCGCGGACCCCGCTGGGGAGCGCACCATGTTGCTGGCCCACTACTGGGGTACT 137  
Db 10877 CCGAGGCGGAGCTGTCTGACGCGAGATTGAAGTCTGACCCCGAGAGACCCGAGCTGG 10818  
Qy 138 GCGCCCGGGAACCGCGGACCCCGGAGCGGCGCATCCACGCGCGGAGCGCGGTGCTGC 197  
Db 10817 TCGGCGCGCGCGCGCGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCTCAGC 10758  
Qy 198 GCTCCG 221  
Db 10757 CCGCCCG 10734

RESULT 11  
US-09-902-540-7886  
; Sequence 7886, Application US/09902540  
; Patent No. 6833447  
GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.

FILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 7886  
; LENGTH: 967  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-7886

Query Match 5.8%; Score 51.4; DB 4; Length 967;  
Best Local Similarity 48.2%; Pred. No. 0.0029;  
Matches 145; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

91 GCTGCGGAGCGCACCGAGCTGTGCTGCGCGCACTACTGCGGGTACTGCGCGGGAAC 150  
Db 3 GCGGCTGAGCCGCGCCAGTGTGAGGCGGAGAGAGAGCGCACCGGTGTGCGCGGAGCT 62  
Qy 151 CGGACCCCGGAGCGCGGCGCATCCAGCGCGGAGCGCGGCTGCGCGCGCGCGCGCGCG 210  
Db 63 TGTACCGAGCGCGGTGTGCGCGCATCCGCGCGCTGCTGCGGCGGTGTGCTGCGAGCGC 122  
Qy 211 CAGGTTACGAGATTCACCGGCTTTTCTCCGCGCTACTCGGCGTACCCGCGGAAACG 270  
Db 123 GCGGCTGCTGCTGCTGCGCGCGCGCGCGCTGTGCGCTGCTGAGAGAGAGCGCGCGCG 182  
Qy 271 CTGAGCTGTGCTGCTGATGAGCGGATTCGCTGCTCCAGACCCCGCGCGCGCGCGCG 330  
Db 183 ATAGCGCTGTGTGTGCTGCGCGCGCGCGCGCTGCGCTGTGCTGAGAGAGAGCGCGCG 242  
Qy 331 GGGAGAGTGTGAGCTGCTGAGCCTTGCAGGAGAGCTGCTGAGAGAGAGCGCGCGTGT 390  
Db 243 CGGAGAGGAGATGCGGAGGAGTGTGCGCGCGCGCGCTGCTGCACTGCTGCGCGCGCG 302  
Qy 391 G 391  
Db 303 G 303

RESULT 12  
US-09-902-540-9238  
; Sequence 9238, Application US/09902540  
; Patent No. 6833447

GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 9238  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-9238

Query Match 5.7%; Score 50.2; DB 4; Length 888;  
Best Local Similarity 46.2%; Pred. No. 0.0056;  
Matches 166; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

17 CGAAGCCCGGCCCCCGGAGAGCGCGGACCATGTTGACGTTGGGGAGCGCACCC 76  
Db 13 GCGCTGAGCTGCGCTGTGAGGAGAGTGTGCGCGGTGTGCTGAGAGAGCGCGAG 72  
Qy 77 ACATGCGGACCGGCTGCGGAGAGCGCACGAGCTGTGCTGCGCGCACTACTGCGGGTAC 136

Db 73 ACGCCCGCGAGGCTCTGAGGTGGCGACGCGAGGGGTGAGAGACTGCTGCTGTCG 132  
Qy 137 TGGCGCCGGGAAACCCGGGACACCCCGAGCGCGCCATCCAGCCCGGCGCGTGTG 196  
Db 133 CCCCTGCGACGACGAGCTGGCGCGGCTTGGGAGATGTGGCGGGCTCTCCG 192  
Qy 197 CGCTCCGCGCGCGCAGGTTACGCGAGATTCAACCGGCTCTTTTCTCCGCTACTCCGC 256  
Db 193 GCCGCTGCGTGGCGGTGATACCGTGTGGCTTCCGCCCTGCTGCTGCTGGCGGCCACT 252  
Qy 257 TACCCCGGAAACCGCTTGAAGTGTGGCGCTGATGGCGAATTCGCTCTCCGACAGC 316  
Db 253 GGGCCCTGCGGTGAGCGGCGCTGGCGCTGCTGCTGAGAGCGTGTGATCATGCTCTC 312  
Qy 317 CCGGCGCCGACCTGGGGGAGAGTGTGACGCTCGTGAACCTTGGCAGGAGAGCTGTGGA 375  
Db 313 TACAGCGCCACCGTGGGCGGTGGCGCGCGCGCTGGCCGAACAGGGGAGCGGCCGA 371

## RESULT 13

US-09-902-540-6388  
; Sequence 6388, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 6388  
; LENGTH: 2199  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-6388

Query Match 5.7%; Score 50.2; DB 4; Length 2199;  
Best Local Similarity 44.6%; Pred. No. 0.0079;  
Matches 196; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

Qy 91 GCTGCGGAGCGCACCGAGCTTCTGCGCGCACTACTGCGGTACTGCGCGCGGGAAC 150  
Db 378 GCTGCTGTGGGCGACGCGCGCGCGCGAGGGCCATCTCCGGGCGCGCGGTGTGCG 437  
Qy 151 CGGCAACCCCGAGCGCGCGCCATTCACGCGCGCGAGCGCGCGTGTGCGCTCCGCGCGC 210  
Db 438 CGGCACTTTCGCGGTGTGCTGTGGGCTTGGCGGACGTAACCGGTGTGCCATGGGCGCT 497  
Qy 211 CAGGTTACGCGAGATTCAACCGGTCTTTTCTCCGCTACTCTGCGCTACCCCGGAAACG 270  
Db 498 CTTCGTCGCGGTGAGGCGCGAGCGCACTGTAACGGGCTGCGCGGAGCGCGCGCA 557  
Qy 271 CTTCGAGCTGTGGCGCTGTATGGGAGATTCCGTGCTCTCCAGACCCCGGCGCACTG 330  
Db 558 GTCCCGCGCTGTGGCGCTGGGGCGCAACCGCGTGTTCACCTTGGCGCGCTGCGCTTCCG 617  
Qy 331 GGGCAGAGTGTGAGCGCTGTGACCTTTCGAGAGAGCGCTGCTGAGAGAGGCGCTGAT 390  
Db 618 GCTGTGGCGCGCTGTGTGAGACATGCGCTCGCGCGCAAGCATATGAGGCGGCGCGG 677  
Qy 391 GACCGCCCGGTGAAAGAAATGGAGCTTTCAGCGCGGCTAAAGAGAGAGAGGAGCGT 450  
Db 678 CAATCTCGGAGGAGGCGGTGCGCGCATGTGCTCCAGATGCGGGGAGGCTCCGGCTACG 737  
Qy 451 CGCCCGGAGACTGCAAGCGCTGTGTGCGCTTGTGAGCTGCGGCTCATGGGCGAGACCG 510  
Db 738 CGACCGGAGCACTTCTTCTGCGCGCGCGGTGTGTGCGCTGATTCGCTGCGCGCGTG 797

Qy 511 CGCCTGCTGAGAGCTCAG 529  
Db 798 GGCCTGGCGCGCGCGCTG 816

## RESULT 14

US-09-902-540-424  
; Sequence 424, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 424  
; LENGTH: 2585  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-424

Query Match 5.7%; Score 50.2; DB 4; Length 2585;  
Best Local Similarity 44.6%; Pred. No. 0.0083;  
Matches 196; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

Qy 91 GCTGCGGAGCGCACCGAGCTTGTGCGCGCACTACTGCGGTACTGCGCGCGGAAAC 150  
Db 716 GCTGCTGTGGGCGACGCGCGCGCGGAGGGCCATCTCCGGGCGCGCGGTGTGCG 775  
Qy 151 CGGCAACCCCGAGCGCGCGCCATTCACGCGCGCGAGCGCGCGTGTGCGCTCCGCGCGC 210  
Db 776 CGGCACTTTCGCGGTGTGCTGTGGGCTTGGCGGACGTAACCGGTGTGCCATGGGCGCT 835  
Qy 211 CAGGTTACGCGAGATTCAACCGGTCTTTTCTCCGCTACTCTGCGCTACCCCGGAAACG 270  
Db 836 CTTCGTCGCGGTGAGGCGCGGACGCACTGTACGGGCTGCGCGGAGCGCGCGCA 895  
Qy 271 CTTCGAGCTGTGGCGCTGTATGGGAGATTCCGTCTCTCCAGACCCCGGCGCACTG 330  
Db 896 GTCCCGCGTGTGGCGCTGTGGGCGCAACCGCGGTGTTCACCTGGGCGCTGTGGGTTCCG 955  
Qy 331 GGGCAGAGTGTGACGCTGTGACCTTTCGAGGAGCGCTGCTGAGAGAGGCGCTGAT 390  
Db 956 GCTGTGGCGCGCTGTGTGAGACATGCGCTCGCGCGCAACGATCAATGCGGCGCAACCGCGG 1015  
Qy 391 GACCGCCCGGTGAAAGAAATGGGCGCTTTCAGCGCGGCTAAAGAGAGAGAGGAGCGT 450  
Db 1016 CAATCTCGGAGGCGCTGCGCGCATGTGCTTCAGATGCGCGGAGCTCCGGCTACG 1075  
Qy 451 CGCCCGGAGACTGCAAGCGCGCTGTGTGCGCTTGTGAGCTGCGGCTCATGGGCGAGACG 510  
Db 1076 CGACCGGAGCACTTCTTCTGCGCGCGCGGTGTGTGCGCTGATTCGCTGCGCGTG 1135  
Qy 511 CGCCTGTGAGAGCTCAG 529  
Db 1136 GGCCTGGGCGCGCGCGCTG 1154

## RESULT 15

US-09-902-540-987  
; Sequence 987, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.



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QY 61 GTTGGGAGAGCGCACACCACTATGCGACCCGCTGCGGAGCGCACCGAGCTGTGCTGAC 120
DB 61 GTTGGGAGAGCGCACACCACTATGCGACCCGCTGCGGAGCGCACCGAGCTGTGCTGAC 120
QY 121 CGACTACTGAGGAGTCTGCGCCCGGGAACCCCGGACCCCGGAGCGCGGCTTCAACGCGC 180
DB 121 CGACTACTGAGGAGTCTGCGCCCGGGAACCCCGGACCCCGGAGCGCGGCTTCAACGCGC 180
QY 181 CGAGGCGCGGCTGCTGCGGCTCCGCGGCGCGCACGAGTTACGAGGATTCACCGGCTCTTTT 240
DB 181 CGAGGCGCGGCTGCTGCGGCTCCGCGGCGCGCACGAGTTACGAGGATTCACCGGCTCTTTT 240
QY 241 CTCGCGCTACCTCGGCTACCCCGGGAACCGCTTCAGAGCTGTGCGCGCTGATGAGCGGATTC 300
DB 241 CTCGCGCTACCTCGGCTACCCCGGGAACCGCTTCAGAGCTGTGCGCGCTGATGAGCGGATTC 300
QY 301 CGTGTCTTCCGACACACCCCGGCGCACTCGGCGGAGAGTGTGAGGCTTGTATCCTTGGC 360
DB 301 CGTGTCTTCCGACACACCCCGGCGCACTCGGCGGAGAGTGTGAGGCTTGTATCCTTGGC 360
QY 361 AGGAGCGCTGCTGAGAGAGGCGCGCTGCTGACCGCGGCTGAGAGAGAGTGTGCGGCTTCCA 420
DB 361 AGGAGCGCTGCTGAGAGAGGCGCGCTGCTGACCGCGGCTGAGAGAGAGTGTGCGGCTTCCA 420
QY 421 GCGCGGCTTAAAGAGAGAGAGGCGAGCTGCGCGGGAATGCGCAGCGCTGTGTGCGCTT 480
DB 421 GCGCGGCTTAAAGAGAGAGAGGCGAGCTGCGCGGGAATGCGCAGCGCTGTGTGCGCTT 480
QY 481 GCTGAGCTTCCGCGCTCACTGCGGCGAGCACCGCGCTGCGAGGCTCAAGGCGGCTTGGGA 540
DB 481 GCTGAGCTTCCGCGCTCACTGCGGCGAGCACCGCGCTGCGAGGCTCAAGGCGGCTTGGGA 540
QY 541 TGGCTTTTGTCACTCTTCAAGGACCCCTTTTTCATGCTGCTTTTGAAGAAACAGCTGGT 600
DB 541 TGGCTTTTGTCACTCTTCAAGGACCCCTTTTTCATGCTGCTTTTGAAGAAACAGCTGGT 600
QY 601 CGAGGCTTTTCTGTATGCTTGTAAACAACAGCTTATATCTCTGAGACAGATTAAT 660
DB 601 CGAGGCTTTTCTGTATGCTTGTAAACAACAGCTTATATCTCTGAGACAGATTAAT 660
QY 661 ATGAGTTTAAACCTTTTAAACCCGCTTCTAAGCTGCGCAACTGTGACCACTTAAATGACAG 720
DB 661 ATGAGTTTAAACCTTTTAAACCCGCTTCTAAGCTGCGCAACTGTGACCACTTAAATGACAG 720
QY 721 ATGTGTGAACAACAAGACTGAGGGAAGACCTTCCCGACCCGACGCTTTTATCTGA 780
DB 721 ATGTGTGAACAACAAGACTGAGGGAAGACCTTCCCGACCCGACGCTTTTATCTGA 780
QY 781 ATGATTAACAAGAGTCTGAGGTGTGATTTGGCAAGTGTAACTTGTGACAGATTAAT 840
DB 781 ATGATTAACAAGAGTCTGAGGTGTGATTTGGCAAGTGTAACTTGTGACAGATTAAT 840
QY 841 CAGGTGTGAAGACAAGATGCAATGCGCTCTTCTTGAAGTGAAGA 887
DB 841 CAGGTGTGAAGACAAGATGCAATGCGCTCTTCTTGAAGTGAAGA 887
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## RESULT 2

US-09-912-599-3

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; Sequence 3, Application US/09912599
; Patent No. US20020106731A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Bcl-2-like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT044P1
; CURRENT APPLICATION NUMBER: US/09/912,599
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/03080
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/179,487
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/180,697
; PRIOR FILING DATE: 2000-02-07
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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-912-599-3
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Query Match 57.1%; Score 506.8; DB 9; Length 522;
Best Local Similarity 99.4%; Pred. No. 7.2e-142;
Matches 519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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QY 270 GCTTCGAGCTGTGCGCGCTGATGCGAGATTCGCTCTCCGACGCGCCGCGCACCT 329
DB 1 GCTTCGAGCTGTGCGCGCTGATGCGAGATTCGCTCTCCGACGCGCCGCGCACCT 60
QY 330 GGGGCAAGTGTGACGCTCGTACCTTCCGAGGAGCGCTGCTGAGAGAGGCGCGCTGG 389
DB 61 GGGGCAAGTGTGACGCTCGTACCTTCCGAGGAGCGCTGCTGAGAGAGGCGCGCTGG 120
QY 390 TGACCGCGCGGTGAGAGAGTGGGGCTTCCAGCGCGGCTTAAAGAGAGAGGCGAGC 449
DB 121 TGACCGCGCGGTGAGAGAGTGGGGCTTCCAGCGCGGCTTAAAGAGAGAGGCGAGC 180
QY 450 TCGCCCGGAGCTGCAGCGCTGTGCTGTGAGCTGCGGCTCATGAGGAGAGCAGC 509
DB 181 TCGCCCGGAGCTGCAGCGCTGTGCTGTGAGCTGCGGCTCATGAGGAGAGCAGC 240
QY 510 GCGCTGCTGCGAGGCTTGAAGGCGGCTGGAGTGGCTTTTGCATCTTTCAGAGCCCT 569
DB 241 GCGCTGCTGCGAGGCTTGAAGGCGGCTGGAGTGGCTTTTGCATCTTTCAGAGCCCT 300
QY 570 TTCACTGCGCTTTTGGAGAAACAGCTGTCCAGGCTTTTCTGTCAATGTTGAACA 629
DB 301 TTCACTGCGCTTTTGGAGAAACAGCTGTCCAGGCTTTTCTGTCAATGTTGAACA 360
QY 630 CAGCTTATTTATCTGTGACAGAGATTTATGAGTTTAAACTTTAAACCGCTTCT 689
DB 361 CAGCTTATTTATCTGTGACAGAGATTTATGAGTTTAAACTTTAAACCGCTTCT 420
QY 690 ACTTCCCAATGTGACCACTTAATGACAAATGTGAGAGAAACAATGAGGGAAGC 749
DB 421 ACTTCCCAATGTGACCACTTAATGACAAATGTGAGAGAAACAATGAGGGAAGC 480
QY 750 ACTTCCCAACCCAGAGC-TTTTATCTGATGATACAA 790
DB 481 ACTTCCCAACCCAGAGCTTTTACTGATGATACAA 522
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## RESULT 3

US-09-764-847-311

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; Sequence 311, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PAM or file wrapper
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 311
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,c,g, or c
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
```

NAME/KEY: SITE  
LOCATION: (26)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (28)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (53)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-847-311

Query Match 51.5%; Score 457.2; DB 9; Length 548;  
Best Local Similarity 98.2%; Pred. No. 6.2e-127;  
Matches 481; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 259 CCCCCGAAACCGCTTCGAGCTGTGTGGCGCTGTATGGCGGATTCGCTCTCCGACAGCCC 318  
DB 61 CCACGCGTCCGGCTTCGAGCTGTGTGGCGCTGTATGGCGGATTCGCTCTCCGACAGCCC 120  
QY 319 CCGCCCCACCTGTGGGCAAGTGTGACGCTGTGACCTTCGACAGGAGCGTGTGAGAG 378  
DB 121 CCGCCCCACCT-GGGCAAGTGTGACGCTGTGACCTTCGACAGGAGCGTGTGAGAG 179  
QY 379 AGGCGCGCTGTGACCGCGCGGTGAAGAGTGGGCTTCAGCGCGCTAAAGAGCA 438  
DB 180 AGGCGCGCTGTGACCGCGCGGTGAAGAGTGGGCGCTTCAGCGCGCTAAAGAGCA 239  
QY 439 GAGAGGCGAGCTGTGCGCCGCGGAGCTGCGACGCTGTGCTGTGAGCTGCGGCTCAT 498  
DB 240 GAGAGGCGAGCTGTGCGCCGCGGAGCTGCGACGCTGTGCTGTGAGCTGCGGCTCAT 299  
QY 499 GGGGACGACCGCGCTGTGCGCTGAGGCTCAGGGCGGCTGGAGTGGCTTTGTCACTTCTT 558  
DB 300 GGGGACGACCGG-CTGTGCTGTGAGCTCAGGGCGGCTGGAGTGGCTTTGTCACTTCTT 358  
QY 559 CAGGACCCCTTTTCCACTGTGCTTTTGGAGAAAACAGCTGTGCAAGCTTTTCTGTATG 618  
DB 359 CAGGACCCCTTTTCCACTGTGCTTTTGGAGAAAACAGCTGTGCAAGCTTTTCTGTATG 418  
QY 619 CTGTTAACAACAGCTTCATTTATCTGTGACACGATTTATTAAGATTAAACCTTTT 678  
DB 419 CTGTTAACAACAGCTTCATTTATCTGTGACACGATTTATTAAGATTAAACCTTTT 478  
QY 679 AACCGGCTTCTACCTGCGCAACTGTGACCACTAAAGACAGATGTGTGAACAAGAC 738  
DB 479 AACCGGCTTCTACCTGCGCAACTGTGACCACTAAAGACAGATGTGTGAACAAGAC 538  
QY 739 TGAGGGAAG 748  
DB 539 TGAGGGAAG 548

## RESULT 4

US-10-092-154-311  
Sequence 311, Application US/10092154  
Publication No. US20030054375A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC009C1  
CURRENT APPLICATION NUMBER: US/10/092,154  
CURRENT FILING DATE: 2002-03-07  
NUMBER OF SEQ ID NOS: 2003  
Prior Application removed - See File Wrapper or Palm  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 311  
LENGTH: 548  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (16)  
OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature  
LOCATION: (20)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (26)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (28)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (53)  
OTHER INFORMATION: n equals a,t,g, or c  
US-10-092-154-311

Query Match 51.5%; Score 457.2; DB 14; Length 548;  
Best Local Similarity 98.2%; Pred. No. 6.2e-127;  
Matches 481; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 259 CCCCCGAAACCGCTTCGAGCTGTGTGGCGCTGTATGGCGGATTCGCTCTCCGACAGCCC 318  
DB 61 CCACGCGTCCGGCTTCGAGCTGTGTGGCGCTGTATGGCGGATTCGCTCTCCGACAGCCC 120  
QY 319 CCGCCCCACCTGTGGGCAAGTGTGACGCTGTGACCTTCGACAGGAGCGTGTGAGAG 378  
DB 121 CCGCCCCACCT-GGGCAAGTGTGACGCTGTGACCTTCGACAGGAGCGTGTGAGAG 179  
QY 379 AGGCGCGCTGTGACCGCGCGGTGAAGAGTGGGCGCTTCAGCGCGCTAAAGAGCA 438  
DB 180 AGGCGCGCTGTGACCGCGCGGTGAAGAGTGGGCGCTTCAGCGCGCTAAAGAGCA 239  
QY 439 GAGAGGCGAGCTGTGCGCCGCGGAGCTGCGACGCTGTGCTGTGAGCTGCGGCTCAT 498  
DB 240 GAGAGGCGAGCTGTGCGCCGCGGAGCTGCGACGCTGTGCTGTGAGCTGCGGCTCAT 299  
QY 499 GGGGACGACCGCGCTGTGCGCTGAGGCTCAGGGCGGCTGGAGTGGCTTTGTCACTTCTT 558  
DB 300 GGGGACGACCGG-CTGTGCTGTGAGCTCAGGGCGGCTGGAGTGGCTTTGTCACTTCTT 358  
QY 559 CAGGACCCCTTTTCCACTGTGCTTTTGGAGAAAACAGCTGTGCAAGCTTTTCTGTATG 618  
DB 359 CAGGACCCCTTTTCCACTGTGCTTTTGGAGAAAACAGCTGTGCAAGCTTTTCTGTATG 418  
QY 619 CTGTTAACAACAGCTTCATTTATCTGTGACACGATTTATTAAGATTAAACCTTTT 678  
DB 419 CTGTTAACAACAGCTTCATTTATCTGTGACACGATTTATTAAGATTAAACCTTTT 478  
QY 679 AACCGGCTTCTACCTGCGCAACTGTGACCACTAAATGACAGATGTGTGAACAAGAC 738  
DB 479 AACCGGCTTCTACCTGCGCAACTGTGACCACTAAATGACAGATGTGTGAACAAGAC 538  
QY 739 TGAGGGAAG 748  
DB 539 TGAGGGAAG 548

## RESULT 5

US-10-363-345A-30995  
Sequence 30995, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
FILE REFERENCE: E01/1227  
CURRENT APPLICATION NUMBER: US/10/363,345A  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 40712  
SEQ ID NO 30995  
LENGTH: 874  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
OTHER INFORMATION: Cpg-island No: 30995  
US-10-363-345A-30995

Query Match 36.6%; Score 324.6; DB 20; Length 874;  
Best Local Similarity 75.1%; Pred. No. 5.9e-87;  
Matches 405; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

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OY 1 CGGGCCAGAAACACGAGGAGGCGCCGCCCGGACGAGGCGGACCATGTTGACCA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 100 CGGGTTAAGAAATTAAGGAGGTTGCGTTTATGTAAGGTCCGATTATGTTGATTA 159
OY 61 GTTGGGAGGCGACACCAATGACCGCTGCGGAGGCGACCGAGCTGTTGCTGAC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 GTTGGGAGGCGATTAATTAATGTCGATTGTTGGGAGGCGATCGATTGTTGCT 219
OY 121 CGACTACCTGGGAGTCTGCGCCCGGAAACCGGACACCCCGAGCGGCGCATCCAGCC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 220 CGATTATTGGGGTATGTCGTTCCGGAATTCTCGATTTTTCAGTCGCGTTATTACGTT 279
OY 181 CGAGGCGCGCTGCTGCGCTCCGCGCGGACGTTACGAGTATTCACCGTCTCTTTT 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 280 CGAGGTGCGTGTGCGTTGCGGTTGCGTTAGTACGTTAGATTATCGGTTTTTTTTT 339
OY 241 CTCGCGCTACCTGCGCTACCCCGGAGACCGCTTCCAGCTGCTGATGCGGATTC 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 340 TTTGCTTATTTTCGTTATTTTCGGAATCGTTTCCAGTTGGTGCGTTGATGCGGATTT 399
OY 301 CGTGTCTCCGACAGCCCGCGCCCACTGCGGAGAGTGTGACGCTGTGACCTTGC 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 400 CGTGTTTTCGATGATTTCGTTTATTTGGGGTGAAGTGAAGTTCGTTGATTTTTCGT 459
OY 361 AGGACGCTGCTGAGAGAGGCGCTGTGACCGCCCGGTGGAAGTGGGGCTTCCA 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 460 AGGACGTTGTTGAGAGAGGCTGCTGTGATGCTTGGTGAAGAGTGGGGTTTTTA 519
OY 421 GCCGCGCTAAAGAGAGAGGCGACGTCGCGCCGCGGACTGCGACGCTTGCGCTT 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 520 GTCCGCGTTAAAGAGTGAAGGCGACGTCGTTGCGGATTTGACGTTTGATGTTT 579
OY 481 GCTGAGCTCGCGCTCATGCGGCGACACCGCGCTGCTGCAAGCTCAAGGCGCGTGG 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 580 GTTGAAGTCGCGGTTATGCGGTTAGTATCGGTTGTTGTTAGGCGGTTGGG 638
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RESULT 6  
US-10-363-345A-30996/c  
Sequence 30996, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
FILE REFERENCE: E01/1227  
CURRENT APPLICATION NUMBER: US/10/363,345A  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 40712  
SEQ ID NO 30996  
LENGTH: 874  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
OTHER INFORMATION: Cpg-island No: 30996  
US-10-363-345A-30996

Query Match 36.6%; Score 324.6; DB 20; Length 874;  
Best Local Similarity 75.1%; Pred. No. 5.9e-87;  
Matches 405; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

```
OY 1 CGGGCCAGAAACACGAGGAGGCGCCGCCCGGACGAGGCGGACCATGTTGACCA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 CGGGTTAAGAAATTAAGGAGGTTGCGTTTATGTAAGGTCCGATTATGTTGATTA 716
OY 61 GTTGGGAGGCGACACCAATGACCGCTGCGGAGGCGACCGAGCTGTTGCTGAC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 715 GTTGGGAGGCGATTAATTAATGTCGATTGTTGGGAGGCGATCGATTGTTGCT 656
OY 121 CGACTACCTGGGAGTCTGCGCCCGGAAACCGGACACCCCGAGCGGCGCATCCAGCC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 CGATTATTGGGGTATGTCGTTCCGGAATTCTCGATTTTTCAGTCGCGTTATTACGTT 596
OY 181 CGAGGCGCGCTGCTGCGCTCCGCGCGGACGTTACGAGTATTCACCGTCTCTTTT 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 CGAGGTGCGTGTGCGTTTCCGCGTCTGTTAGGTTACGTTAGATTATCGGTTTTTTTTT 536
OY 241 CTCGCGCTACCTGCGCTACCCCGGAGACCGTTTGACCTGTGTGCGCTGATGCGGATTC 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 TTTGCTTATTTTCGTTATTTTCGGAATCGTTTGAAGTTGGCGTTGATGCGGATTT 476
OY 301 CGTGTCTCCGACAGCCCGCGCCCACTGCGGAGAGTGTGACGCTGTGACCTTGC 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 CGTGTTTTCGATGATTTCGTTTATTTGGGGTGAAGTGAAGTTCGTTGATTTTTCGT 416
OY 361 AGGACGCTGCTGAGAGAGGCGCTGTGACCGCCCGGTGGAAGTGGGGCTTCCA 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 415 AGGACGTTGTTGAGAGAGGCGTGTGTTGATGCTTCGTTGGAAGTGGGGTTTTTA 356
OY 421 GCCGCGCTAAAGAGAGGCGACGTCGCGCGGAGCTGCAAGGCGCTTGCGCTT 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 355 GTCCGCGTTAAAGAGTGAAGGCGACGTCGTTGCGGATTTGTAAGCTTGGGTTTTT 296
OY 481 GCTGAGCTCGCGCTCATGCGGCGGACACCGCGCTGCGTCAAGGCGCGCTGGG 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 GTTGAAGTCGCGGTTATGCGGTTAGTATCGGCTTGGTTGAGGTTTAGGCGGTTGG 237
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RESULT 7  
US-10-363-345A-30993/c  
Sequence 30993, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
FILE REFERENCE: E01/1227  
CURRENT APPLICATION NUMBER: US/10/363,345A  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 40712  
SEQ ID NO 30993  
LENGTH: 874  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
OTHER INFORMATION: Cpg-island No: 30993  
US-10-363-345A-30993

Query Match 36.1%; Score 320; DB 20; Length 874;  
Best Local Similarity 74.8%; Pred. No. 1.4e-85;  
Matches 401; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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OY 1 CGGGCCAGAAACACGAGGAGGCGCCGCCCGGACGAGGCGGACCATGTTGACCA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 CGAACCAAAAACCAAGAAACCCGACCCCAACAAAACCGAACCAATTAATTAACCA 716
OY 61 GTTGGGAGGCGACACCAATGACCGCTGCGGAGGCGACCGAGCTGTTGCTGAC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 715 ATTGAGAAAGGACACCAATTAACCGCTGTCGAAAGGACCGGAATTAATTAATTAAC 656
OY 121 CGACTACCTGGGAGTATGCGCCCGGAGAACCGGACACCCCGAGCGGCGCATCCAGCC 180
```

Db 655 CGACTACCTAAATATCTACGCGCGGAAACCCGACACCCCGGAAACCGAGCCGATTCACGCGC 596  
Qy 181 CGAGGCGCGCGCTGCTGCGCTCCGCGCGCGGCGGAGTTAGGAGATTACCGGCTCTTTT 240  
Db 595 GGAACCGCGCTACTACGCTCCGCGCGGCGGAAATTAAGACAAATTAACCGATCTCTTTT 536  
Qy 241 CTCGCGCTACCTCGGCTACCGCGGGAACCGCTTGAGCGTGGTGGGCTGATGGGATTC 300  
Db 535 CTCGCGCTACCTCGGCTACCGCGGGAACCGCTTGAGCGTGGTGGGCTGATGGGATTC 476  
Qy 301 CGTCTCTCGGACAGCGCGCGCGCGCGCGGCGGAGTGTGAGCTGAGCTGAGCTTCGC 360  
Db 475 CGTACTCTCGGACAGCGCGCGCGCGCGCGGCGGAGTGTGAGCTGAGCTGAGCTTCGC 416  
Qy 361 AGGAGCGTGTGAGAGAGAGGCGCGCTGTGAGCGCGCGCGGCGGAGTGTGAGCTTCGA 420  
Db 415 AAAACCGTACTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 356  
Qy 421 GCCGCGCTAAAGAGAGAGAGGCGAGCGTGGCGCGCGGAGTGTGAGCTGAGCTTCGCCTT 480  
Db 355 ACCGCGCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 296  
Qy 481 GCTGAGCTCGGCGCTCATGAGGCGAGCACCGCGCGCTGCTGAGCTGAGCGCGCT 536  
Db 295 ACTAACTCGGCGCTCATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 240

RESULT 8  
US-10-363-345A-30994  
; Sequence 30994, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363,345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 30994  
; LENGTH: 874  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: Cpg-Island No: 30994  
US-10-363-345A-30994

Query Match 36.1%; Score 320; DB 20; Length 874;  
Best Local Similarity 74.8%; Pred. No. 1.4e-85;  
Matches 401; Conservative 0; Mismatches 135; Indels 0; Gaps 0;  
Qy 1 CGGCGCAAGAAACAGGAGCG 60  
Db 100 CGAAGCAAAACCAAGAAACCGGAGCG 159  
Qy 61 GTTGCGGAGCGCAACCATGCG 120  
Db 160 ATTGAGAAAGCAACCATGCG 219  
Qy 121 CGACTACTGAGGATGCTGCG 180  
Db 220 CGACTACTGAGGATGCTGCG 279  
Qy 181 CGAGGCGCGCGTGTGCG 240  
Db 280 CGAAGCGCGCTACTGCG 339  
Qy 241 CTCGCGCTACCTCGGCTACCGCGGGAACCGCTTGAGCGTGGTGGGCTGATGGGATTC 300

Db 340 CTCGCGCTACCTCGACTACCGCGGAAACCGCTTGAACTAATAAGCTAATAAGCAATTC 399  
Qy 301 CGTCTCTCGGACAGCG 360  
Db 400 CGTACTCTCGGACAGCG 459  
Qy 361 AGGAGCGTGTGAGAGAGAGGCGCGTGTGAGCGCGCGCGGCGGAGAGTGGGCTTCGA 420  
Db 460 AAAACCGTACTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 519  
Qy 421 GCCGCGCTAAAGAGAGAGGCGAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 480  
Db 520 ACCGCGCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 579  
Qy 481 GCTGAGCTCGGCGCTCATGAGGCGAGCACCGCGCGCTGCTGAGGCTGAGGCGCGCT 536  
Db 580 ACTAACTCGGCGCTCATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 635

RESULT 9  
US-09-908-975-15549  
; Sequence 15549, Application US/0908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: MASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchaon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15549  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-15549

Query Match 6.8%; Score 60; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 8.9e-08;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 565 CCCCTTCCACTGCTTTTGGAGAAACAGCTGTGAGGCTTTTCTGTATGCTGTT 624  
Db 1 CCCCTTCCACTGCTTTTGGAGAAACAGCTGTGAGGCTTTTCTGTATGCTGTT 60  
RESULT 10  
US-10-338-110-119  
; Sequence 119, Application US/10338110  
; Publication No. US20040023254A1  
; GENERAL INFORMATION:  
; APPLICANT: Fuhrmann, Jeffrey J.  
; APPLICANT: Romesser, James A.  
; TITLE OF INVENTION: A Method To Assess Quorum Sensing Potential Of Microbial  
; FILE REFERENCE: HSR-0056  
; CURRENT APPLICATION NUMBER: US/10/338,110  
; CURRENT FILING DATE: 2003-01-07  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 119  
; LENGTH: 536  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

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FEATURE:
OTHER INFORMATION: Consensus Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(7)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: n is a, c, g, or t
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OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
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OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
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OTHER INFORMATION: n is a, c, g, or t
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OTHER INFORMATION: n is a, c, g, or t
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FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (509)..(509)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (517)..(517)
OTHER INFORMATION: n is a, c, g, or t
US-10-338-110-119
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Query Match 6.3%; Score 56; DB 17; Length 536;  
Best Local Similarity 15.2%; Pred. No. 3.3e-06;  
Matches 61; Conservative 194; Mismatches 144; Indels 1; Gaps 1;

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Qy 118 GAGCGACCTGAGGTAAGCGGAGACCGGAGCGCGCCATTCAC 177
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|
Db 129 SSKTACTSBSGSHVKGWVYVGBDHTSKTGGHVGSGSCSCTGHTMCCAC 188
Qy 178 GCCGAGGCGCGGTGCTGCCGCGCGCGAGTTACGAGATTCAACGGTCTT 237
```

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Db 189 SACVBDSBCEWAYCTGCTBBAARKVNSVTYTYRS-BMYNSBKCBVSRVMMTRCCSM 247
    :|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 238 TTCTCCGCCCTACCTGAGTACCCCGGGAACCGCTTGAGTGGCTGATGGCGA 297
    |||::|::|::|::|::|::|::|::|::|::|::|::|
Db 248 VSVATCCVKMSRTYTGGAHTKWCNCGMTWCRSCRCRHSAMTKGSGSRGMV 307
Qy 298 TTCGTGCTCTCCAGACGCCCGGCCCACTGGAGGAGTGTGACGCTGTACCTT 357
    ::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 308 KMTYTSKSDVMHBCSTVARMGSDSYWVBSGNGCVRKXVNTSRTSGSVRY 367
Qy 358 CGCAGGACGCTGCTGAGAGAGGCGCGCTGTGACCGCCGCTGGAAGAAGTGGGCTT 417
    ::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 368 SRYSWHCRBSRSXATGVMGGSYKWTWCVDNMKSAMCGBRVWDSBSHNSANGSVYGG 427
Qy 418 CCAGCCGGGCTAAAGAGAGGAGGAGGAGCTGCCCGGACTGCGAGCGCTGTGAC 477
    ::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 428 BYCSYEMHSMVMMVRRBRBDMHRTSSISGSGTSTYGGAYCRVADCRMDSCVYVM 487
Qy 478 CTTCGTAGCTCGCGGCTCATGGGAGACACCGGCGCTGG 517
    :|::|::|::|::|::|::|::|::|::|::|::|::|
Db 488 SVHBYKXWCKYXRSMHYCVNRHBBGVBMVYKXVVG 527
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RESULT 11  
US-10-437-963-2495  
Sequence 2495, Application US/10437963  
Publication No. US2004012343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Mu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 2495  
LENGTH: 989  
TYPE: DNA  
ORGANISM: *Oryza sativa*  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102262C.1  
US-10-437-963-2495

Query Match 6.2%; Score 55.2; DB 19; Length 989;  
Best Local Similarity 48.1%; Pred. No. 7.3e-06;  
Matches 156; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

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Qy 68 GAGCGACACCATGATCGGACCGCTGCGGAGCGACCGAGCTGTGCTGCGCACTAC 127
    |||::|::|::|::|::|::|::|::|::|::|::|::|
Db 279 GACGCAACCGTGCCTGCGACCACTCCACAACTTCAGACGCGTCCATCTCCCTCGCG 338
Qy 128 CTGGGTAATCGCGCGGGAACCGGCAACCGGAGCGCGCATCAGCGCGGAGGCC 187
    |||::|::|::|::|::|::|::|::|::|::|::|::|
Db 339 CTGCTGCTAAGCGCGCGCGCGCGCGCTTCGACGTGGCGCGGAGCGCGAGCGCGC 398
Qy 188 GCCGAGTGGCTGCGCGCGCGCGCGAGGTTACGAGATTACCGGTCCTTTCTCCGCC 247
    |||::|::|::|::|::|::|::|::|::|::|::|::|
Db 399 GCGGTGCGAGCTGTCGCGCGCGCGCGCTGCGCGAGCGAGTCTGTTCACTGC 458
Qy 248 TACCTGCTAACCCCGGGAACCGCTTGAAGTGGCGCTGATGGCGGATTCGCTGCTC 307
    |||::|::|::|::|::|::|::|::|::|::|::|::|
Db 459 CACTCGGAGGACCAAGCGGAGGTGAAGGAGCACTGCTGTCGAGGAGGTGCTG 518
Qy 308 TCCGACAGCCCGGCGCGCGCTGGGAGAGTGTGACGCTGTCGACCTTGCGAGGAGCG 367
    |||::|::|::|::|::|::|::|::|::|::|::|::|
```

```
Db 519 GCCGTACGCTGCGCGGACGAGTGTGCGGCTGCGCGCCGACGAGCTTCGGGTGAGC 578
Qy 368 CTGCTGAGAGAGGCGCGTGTG 391
Db 579 CTCGTGCGGTGCGGACGCTGTGTG 602

RESULT 12
US-10-106-534-3
; Sequence 3, Application US/10106534
; Publication No. US2002016868A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 14691. A Human Glutamate Receptor Family
; TITLE OF INVENTION: Member and Uses Therefor
; FILE REFERENCE: MP101-042P1RM
; CURRENT APPLICATION NUMBER: US/10/106,534
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/279,086
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2997)
US-10-106-534-3

Query Match 6.2%; Score 55.2; DB 13; Length 2997;
Best Local Similarity 48.4%; Pred. No. 1.1e-05;
Matches 185; Conservative 0; Mismatches 193; Indels 4; Gaps 1;

Qy 82 GACCGACCCGCTGCGGAGCGGACCGAGCTGTGCGGCGGACTGAGGCTGAGTGTGCGC 141
Db 145 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 204
Qy 142 CCGGGAACCGGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 201
Db 205 AACCTGAGCTTGTGAGCTGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 264
Qy 202 CCGCGCGCGCGGAGTGTGAGCTGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 261
Db 265 CCGCGCGCGGTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 320
Qy 262 CCGGGAACCGCTTGTGAGCTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 321
Db 321 CGAGGCTGCGCGCGGAGCTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 380
Qy 322 CCGGCACTGTGAGGAGTGTGTGAGCTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 381
Db 381 GCTGAGCTGTGCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
Qy 382 GCGCGTGTGAGCGGCGGCGGAGAGTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 441
Db 441 CCGCGTGTGAGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 500
Qy 442 GGGGAGCTGCGCGGCGGAGTGC 463
Db 501 CGTGGCTGTGCGCGCTGTGCGCG 522

RESULT 13
US-10-106-534-1
; Sequence 1, Application US/10106534
; Publication No. US2002016868A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 14691. A Human Glutamate Receptor Family
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; TITLE OF INVENTION: Member and Uses Therefor
; FILE REFERENCE: MP101-042P1RM
; CURRENT APPLICATION NUMBER: US/10/106,534
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/279,086
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3158
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2997)
US-10-106-534-1

Query Match 6.2%; Score 55.2; DB 13; Length 3158;
Best Local Similarity 48.4%; Pred. No. 1.1e-05;
Matches 185; Conservative 0; Mismatches 193; Indels 4; Gaps 1;

Qy 82 GACCGACCCGCTGCGGAGCGGACCGAGCTGTGCGGCGGACTGAGGCTGAGTGTGCGC 141
Db 145 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 204
Qy 142 CCGGGAACCGGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 201
Db 205 AACCTGAGCTTGTGAGCTGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 264
Qy 202 CCGCGCGCGCGGAGTGTGAGCTGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 261
Db 265 CCGCGCGCGGTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 320
Qy 262 CCGGGAACCGCTTGTGAGCTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 321
Db 321 CGAGGCTGCGCGCGGAGCTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 380
Qy 322 CCGGCACTGTGAGGAGTGTGTGAGCTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 381
Db 381 GCTGAGCTGTGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
Qy 382 GCGCGTGTGAGCGGCGGCGGAGAGTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 441
Db 441 CCGCGTGTGAGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 500
Qy 442 GGGGAGCTGCGCGGCGGAGTGC 463
Db 501 CGTGGCTGTGCGCGCTGTGCGCG 522

RESULT 14
US-10-425-115-143369
; Sequence 143369, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 143369
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MNT4577_6222C.1
US-10-425-115-143369
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Size-selected on agarose gel. Average insert size ~1kb. 5' xhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

## ORIGIN

Query Match 32.6%; Score 289.4; DB 6; Length 715;

Best Local Similarity 93.5%; Pred. No. 1.8e-60;

Matches 302; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY CCCCCTTTCACCTGCTTTTGGAGAAACAGCTGCTTCTTCTGATGCTGTT 624  
DB CCCCCTTTCACCTGCTTTTGGAGAAACAGCTGCTTCTTCTGATGCTGTT 648  
QY AACACAGCCTTCACTTATCTCTGACACGATTTATGATTTTAAACCTTTAACCCG 684  
DB ACCACACGCTCATTTATCTCTGACACGATTTATGATTTTAACTTTTACCCCG 588  
QY CTTTACCTGCTTCACTGCTTGAACCACTAAATGACATGCTGAGAACAGACTGAGG 744  
DB CTTACCTGCTTCACTGCTTGAACCACTAAATGACATGCTGAGAACAGACTGAGG 528  
QY AAAGACCTTCCCTCCACCCAGACGCTTTTATCTGAATGACATACAGAGAGCTGAGGTG 804  
DB AAAGACCTTCCCTCCACCCAGACGCTTTTATCTGAATGACATACAGAGAGCTGAGGTG 468  
QY GTGATTTGGCCAGTGTTTTAACTTGTGACAGTGTGAGAGCAAGATGCAAA 864  
DB GTGATTTGGCCAGTGTTTTAACTTGTGACAGTGTGAGAGCAAGATGCAAA 408  
QY TGGCTCTCTCTTGAAGTGAAGA 887  
DB TGGCTCTCTCTTGAAGTGAAGA 385

RESULT 2  
LOCUS BG080862 626 bp mRNA linear EST 17-DEC-2003  
DEFINITION H3058C03-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone  
H3058C03 5', mRNA sequence.  
ACCESSION BG080862  
VERSION BG080862.2 GI:40014930  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 626)  
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Fiao,Y., Nagataja,K., Doi,H., Wood,W.H., III, Becker,K.G. and Ko,M.S.H.  
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray  
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)  
20381348  
10922068  
COMMENT On Jan 26, 2001 this sequence version replaced gi:12563419.  
Other ESTs: H3058C03-3  
Contact: George J. Kargul  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
This clone set has been freely distributed to the community. Please visit <http://1gsun.grc.nia.nih.gov/cDNA/15k.html> for details.  
Plate: H3058 row: C column: 03  
Seq primer: -21M13 Reverse  
High quality sequence stop: 626  
POLYA=No.

## FEATURES

Location/Qualifiers

## source

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/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:H3058C03-5"  
/db\_xref="taxon:10050"  
/clone="H3058C03"  
/sex="Clones arrayed from a variety of cDNA libraries"  
/dev\_stage="Clones arrayed from a variety of cDNA libraries"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse 15K cDNA Clone Set"  
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryo, extraembryonic part of E7.5 embryo, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

## ORIGIN

Query Match 26.6%; Score 236.2; DB 4; Length 626;  
Best Local Similarity 65.1%; Pred. No. 2.4e-47;  
Matches 407; Conservative 0; Mismatches 193; Indels 25; Gaps 3;

QY GACCCGCTGCGGAGCCGACGAGCTGTGCTGCGCCGACTACGAGGTACTGCGCCG 145  
DB GACCCGCTGCGGAGCCGACGAGCTGTGCTGCGCCGACTACGAGGTACTGCGCCG 77  
QY GACCCGCTGCGGAGCCGACGAGCTGTGCTGCGCCGACTACGAGGTACTGCGCCG 205  
DB GACCCGCTGCGGAGCCGACGAGCTGTGCTGCGCCGACTACGAGGTACTGCGCCG 137  
QY GCGCGAGCTTACGCGGATTCACCGGCTTTTCTCCGCTACCTGCGCTACCGCGG 265  
DB GCGCGAGCTTACGCGGATTCACCGGCTTTTCTCCGCTACCTGCGCTACCGCGG 197  
QY AACGCTTGCAGCTGTGCGCTGATGCGGATTCGCTCTCCGACAGCCCGCGCC 325  
DB AACGCTTGCAGCTGTGCGCTGATGCGGATTCGCTCTCCGACAGCCCGCGCC 257  
QY ACTGCGGAGAGTGTGATCGCTGTGACCTTCCGAGGAGCTGTGAGAGAGGCGG 385  
DB ACTGCGGAGAGTGTGATCGCTGTGACCTTCCGAGGAGCTGTGAGAGAGGCGG 317  
QY AGCTGAGCCCACTGTGTATCTCTGCGCTTCCGCGGAGAGCTTAATCAAGGCGCT 445  
DB AGCTGAGCCCACTGTGTATCTCTGCGCTTCCGCGGAGAGCTTAATCAAGGCGCT 359  
QY TACATGCTGTGACAGCAACA-----GGAATCGGGAATCTGTCTC 502  
DB TACATGCTGTGACAGCAACA-----GGAATCGGGAATCTGTCTC 419  
QY GACGTCGCGCGGAGCTGCGACGCTGTGCTGTGACCTGCGGCTCATGCGG--- 562  
DB GACGTCGCGCGGAGCTGCGACGCTGTGCTGTGACCTGCGGCTCATGCGG--- 479  
QY CAGGACCGCGCTGCTGCGAGCTGAGGCGCGCTGAGGAGCTTTTGTACCTTTCAG 622  
DB CAGGACCGCGCTGCTGCGAGCTGAGGCGCGCTGAGGAGCTTTTGTACCTTTCAG 539  
QY ACCGCTTTCACCTGCTTTTGGAGAAACAGCTGTGCTGAGGCTTTTCTGATGCTTG 622  
DB ACCGCTTTCACCTGCTTTTGGAGAAACAGCTGTGCTGAGGCTTTTCTGATGCTTG 539

QY 623 TTAACAAGACGCTTATCTGACACGATTATATGAGTTTAAACTTTAAC 682  
DB 540 TTTCGAAGAGCCATCTTTTATCTGGAACGTTAT-----AAGTTTAAATTTTAAAG 595  
QY 683 CGCTTCTACCTGCCCACTGTGACC 707  
DB 596 CGATCTTACTTACTTACTGTAAC 620

RESULT 3  
LOCUS CO798715 875 bp mRNA linear EST 05-AUG-2004  
DEFINITION AGENCOURT 30259012 NIH\_MGC\_256 Mus musculus cDNA clone  
IMAGE:30935405 5', mRNA sequence.  
ACCESSION CO798715  
VERSION CO798715.1 GI:50986895  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 875)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Kathleen Horner, Stanford University  
cDNA Library Preparation: Express Genomics  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDAM189 row: h column: 06  
High quality sequence stop: 659.  
Location/Qualifiers  
1. 875  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/clone="IMAGE:30935405"  
/lab\_host="DH10B TONa"  
/clone\_lib="NIH\_MGC\_256"  
/note="Organ: oocyte; Vector: pExpress-1; Site: 1: EcoRV,  
Site 2: NotI; cDNA was primed using oligo-dT primer:  
5'-pGACATGTTCTAGATCGGAGCGCGGCC(7)25-3' and cloned into  
the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb  
resulted in an average insert size of 1.2 kb. This is a  
primary library (normalized primary library is NIH\_MGC\_257)  
and was constructed by Express Genomics (Frederick, MD).  
Note: this is a NIH\_MGC library"

ORIGIN  
Query Match 26.5%; Score 235.4; DB 7; Length 875;  
Best Local Similarity 64.2%; Pred. No. 4,1e-47;  
Matches 414; Conservative 0; Mismatches 206; Indels 25; Gaps 3;

QY 86 GACCCGCTGCGGAGACGACCGAGCTGTTGCTGGCCGACTACTGGGGTACTGGCCCGG 145  
DB 27 GACCCACTGCAATGAACGACTAGACGGCTGCTGTGACTACATATTTCTTGGCCACGG 86  
QY 146 GAACCCGGACACCCCGAGCCGCGCATTCACAGCCGAGCGCGCTGCTGCGTCCGG 205  
DB 87 GAGCCGACACCCCGAGACGACCGCCCACTGTCTGTGAGCGCGCTTGTGCTCTGTG 146  
QY 206 GCCGCAAGTTACGCGAGATTTCACCGGTCCTTTTCTCGGCTTACTCGGCTACCCCGG 265  
DB 147 ACTAGGAGATTCACAGAGACCAAGAAATTTTCTCTCTCTGCGAAGCCGCGGCG 206

QY 266 AACCGCTTCAGCTGTGCGCGCTGATGCGGATTCCTGCTCTCGACAGCCCGGCC 325  
DB 207 AATGCCCTGAGCTGTGTAAACAGATGGCAGATTAAGTGTCTCTCCAAAGCAAGACTTC 266  
QY 326 ACCTTGGGACAGATGTGTACGCTGTAACCTTTCCGAGGAGCGCTGTGAGAGAGCGG 385  
DB 267 AGCTGAGACCAACTGTGTATCTCTGTGCTTCGCGGGGAGCGCTTATATCAAGCCCT 326  
QY 386 CTGTGACCGCCCGGTGAGAGATGTGGGCTTCCAGCCGCGCTTAAAGAGAGAGGGC 445  
DB 327 TACATGCTGTTCACAGAGAG-----GGAGTCTGGAGATGCTTC 368  
QY 446 GACGTGCCCGGAGACTGCGACGCGCTGTGCTGTGAGCTGCGCGCTCAATGGG--- 502  
DB 369 ATAGTGACCCAGACACTGTGTCTATAGTGAACCTTCTGTATATCTGTCTATGGGGGT 428  
QY 503 CAGACCGCGCTGTGCTGACAGGCTTCAGGGCGGCTGTGGATGTGCTTGTCACTTTCAG 562  
DB 429 CGGACCGCGCGAGGCTGAGAGGCTCTCGCGCGGCTGTGGATGTGCTTTCCTTCAAG 488  
QY 563 ACCCGCTTTCAGCTGTGCTTTTGGAGAAACAGCTGTGCGAGCTTTCGTGANTGTG 622  
DB 489 AATCTTACCGCTGTGCTTCTGAGAAAGATTGCTGATTCAGGCTTCTGTGAGGCTTC 548  
QY 623 TTAACAAGACGCTTATCTGACACGATTATATGAGTTTAAACTTTAAC 682  
DB 549 TTTCGAAGAGCCATCTTTTATCTGGAACGTTAT-----AAGTTTAAATTTTAAAG 604  
QY 683 CGCTTCTACCTGCCCACTGTGACCACTAAATGACAGATGTG 727  
DB 605 CGATCTTACTTACTTACTGTAACCTCTGTAAGAACTTCGGG 649

RESULT 4  
LOCUS CF915355 649 bp mRNA linear EST 05-NOV-2003  
DEFINITION B0978E08-5 NIA Mouse Unfertilized Egg cDNA Library (long 1) Mus  
musculus cDNA clone NIA:B0978E08 IMAGE:30479767 5', mRNA sequence.  
ACCESSION CF915355  
VERSION CF915355.1 GI:38186557  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 649)  
AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
TITLE Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)  
MEDLINE 21429098  
PUBMED 11544199  
COMMENT Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: [cdna@gsun.grc.nia.nih.gov](mailto:cdna@gsun.grc.nia.nih.gov)  
Plate: B0978 row: B column: 08  
Seq primer: M13 Reverse  
High quality sequence stop: 649  
POLY-A-No.  
Location/Qualifiers  
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/db\_xref="taxon:10090"  
/clone="NIA:B0978E08 IMAGE:30479767"  
/dev\_stage="Unfertilized Egg"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Unfertilized Egg cDNA Library (long

1)"  
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;  
Site 2: NotI; Mouse cDNA project by the Laboratory of  
Genetics, National Institute on Aging (NIA), Intramural  
Research Program, NIH (http://nigam.gtc.nia.nih.gov/cDNA).  
This is a long-transcript enriched cDNA library (Ref.  
Genome Res. 11: 1553-1558 (2001). [PMD: 1154191]). Total  
RNAs were extracted from a pool of 148 unfertilized eggs.  
Double-stranded cDNAs were synthesized with an Oligo(dT)  
primer (Invitrogen):  
5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT-3',  
treated with T4 DNA polymerase, and purified by  
ethanol-precipitation. The cDNAs were ligated to  
lone-linker lI-SalI, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer SalI-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid  
vector. The DH10B E. coli host was transformed with the  
ligation mixture by the standard chemical method. The  
average insert size is about 2.5 kb. The library was  
constructed by Yulan Piao."

## ORIGIN

Query Match 26.5%; Score 235.2; DB 7; Length 649;  
Best Local Similarity 64.4%; Pred. No. 4,3e-47;  
Matches 412; Conservative 0; Mismatches 203; Indels 25; Gaps 3;

86 GACCCGCTGCGGAGCGACCGAGCTGTGTGCGCGACTACCTGGGGTACTGCGCCGG 145  
18 GACCCACTGCATGAAAGCGACTAGACGGCTGTGTGACTATATTTCTTGGCCACGG 77  
146 GAACCCGCGACCCCGGAGCGGCGGCTATCAGCCCGAGCGCGCGCTGCTCCGG 205  
78 GAGCCGGAACCCCGAGCGCCCAAGTGTGTGAGCGCGCGCTTGTGCTCTGTG 137  
206 GCCCGCAGTTACGGCAGATTCACCGGCTCTTTTCTCCGCTACTCGGGTACCCCGG 265  
138 ACTAGGCGAGATCAAGAGAGACCAAGATTTTCTCTCTTCTCCGAAACCGCGGC 197  
266 AACCCCTTGAAGCTGTGCGCTGATGTGCGGATTCGCTCTCCGACAGCCCGCGCC 325  
198 AATGCCCTGAGCTGTGTAACAGATGAGATAGTTGCTTCCAAAGACCAAGACTTC 257  
326 ACCTGGGCGAGAGTGTGACGCTGATCTTGTGCGAGGACCTGTGCGAGAGGCGCG 385  
258 AGCTGAGGCAACTGTGTCTCTCTGCGCTTCCGCGGAGCGCTTATGATCAAGGCGCT 317  
386 CTGGTGACCGCGGCGGAGAGAGTGGGCTTCCAGCGCGCGCTAAAGAGAGAGGCGC 445  
318 TACATGGCTGTCAAGCAAGAG-----GGGATCTGGGGAATGCTGTTC 359  
446 GACCTGCGCCGGAGATGCGAGCGCTGTGAGCTTGTCTGAGCTCGCGGCTCAATGGG-- 502  
360 AATAGTACCGGAGACGCTGTCTCATATGAACTTTCTGTATATCTGTCTATGGGGCT 419  
503 CAGCACCGGCGCTGCTGAGGCTCAGGGCGGCTGGATGCTTTTGTACTTTCTTCAAG 562  
420 CGGCAACCGGCGGAGGCTGTGCGCGGCTGGGATGCTTTTGTGCGCTTCTTCAAG 479  
563 ACCCCCTTTCAGCTGGCTTTTGGAGAAACAGCTGTGCTCAGGCTTTTGTCAATGCTTG 622  
480 AATCTTTTACGCTCGGCTTGTGAGAGATGCTGATTCAGGCTTTTGTCAAGCTTTC 539  
623 TTAAACAAGCCTTATTTATCTGAGACAGATTAATTAATGATTTTAACTTTTAAAC 682  
540 TTTGGAAGGCACTTTTATATCTGAAACGTTAT---AAGTTAAATTTTAAAG 595  
683 CGCTTCTACTGCGCACTGTGACCACTAATGACAGT 722  
596 CGATCTTACTTACTTACTGTGAACCTCTAAGAGACAAAT 635

RESULT 5  
LOCUS COB14648 772 bp mRNA linear EST 06-AUG-2004  
DEFINITION AGNCOURT 30246837 NIH\_MGC 256 Mus musculus cDNA clone  
IMAGE:30937746 5', mRNA sequence.  
ACCESSION COB14648  
VERSION COB14648.1 GI:51033274  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
TITLE Contact: Daniela S. Gerhard, Ph.D.  
COMMENT Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cga@db-remail.nih.gov  
Tissue Procurement: Dr. Kathleen Horner, Stanford University  
CDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNU)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNU at:  
http://image.llnl.gov  
Plate: NDM1195 row: 1 column: 19  
High quality sequence start: 5  
High quality sequence stop: 666.  
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/clone="IMAGE:30937746"  
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/clone\_lib="NIH\_MGC\_256"  
/note="Organ: oocyte; Vector: pExpress-1; Site 1: EcoRV;  
Site 2: NotI; cDNA was primed using oligo-dT primer:  
5'-pGACTAGTCTTCAATCGGAGCGCGCGGCTGTAATTCCTTCTGCGGCGGCG 101  
the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb  
resulted in an average insert size of 1.2 kb. This is a  
primary library (normalized primary library is NIH\_MGC 257)  
and was constructed by Express Genomics (Frederick, MD).  
Note: this is a NIH\_MGC library"

## FEATURES

source

## ORIGIN

Query Match 26.3%; Score 233.4; DB 7; Length 772;  
Best Local Similarity 63.9%; Pred. No. 1.2e-46;  
Matches 412; Conservative 0; Mismatches 208; Indels 25; Gaps 3;

86 GACCCGCTGCGGAGCGACCGAGCTGTGTGCGCGACTACCTGGGGTACTGCGCCGG 145  
42 GACCCACTGCATGAAAGCGACTAGACGGCTGTGACTTCAATATCTTCTGCGGCGAG 101  
146 GAACCCGCGACCCCGGAGCGGCGGCTATCAGCGCGGAGCGCGCGCTGCTGCGCG 205  
102 GAGCCGGAACCCCGAGACCAACCGCCAGCTGTGTGAGGCGGCGCTTCTGCTGTG 161  
206 GCCCGCAGTTACGGCAGATTCACCGGCTTTTCTCCGCTACTCGGGCTACCCCGG 265  
162 ACTAGGCGAGATCAAGAGAGACCAAGATTTTCTCTCTTCTTGTGAGAAAGCGGGG 221  
266 AACCCCTTGAAGCTGTGAGCGCTGATGTGCGGATTCGCTCTCGACAGCCCGCGCC 325  
222 AATGCCCTGAGCTGTGTAACAGATGCAATAGTTGCTCTCAAGACCAAGACTTTC 281  
326 ACCTGGGCGAGAGTGTGACGCTGTGACCTTTCGAGGAGAGCTGTGAGAGAGGCGCG 385

Db 282 AGCTGAGCAACGCTGATGCTCTGAGCTTCGCGGGAGACGCTTATGATCAAGGCCCT 341  
 Oy 386 CTGGAGACCGCCCGGTGAAGAAGTGGGCTTCACGCCGCTAAAGACGAGAGGC 445  
 Db 342 TACATGGCTGTCAACAGAAAG-----GGGATCTGGGGATCGTGC 383  
 Oy 446 GACCTGCGCCGGGACCTGACGAGCGCTGGTGCCTTGTGAGTCCGCGCTCAATGGGG-- 502  
 Db 384 ATAGAGACCCGAGACTGCTGTCTCATAGTGAACCTTCTGTATATATCTGTCTATGGGGCGT 443  
 Oy 503 CAGCAGCCGCGCTGCTGACAGGCTGACGGCGGCTGGATGCGCTTTGTCACTTCTTCAG 562  
 Db 444 CGGACACCCCGCAGGCTGAGAGGCTCTCGCGGCTGGATGCGCTTTGCGGCTTCTTCAAG 503  
 Oy 563 ACCCGCTTTCACGCTGCTTTTGGAGAAACAGCTGCTCCAGGCTTTTCTGTCAGCTTG 622  
 Db 504 AATCTTTACGCTGCTGCTTGGAGAAAGATTGCGATTCAGGCTTTCTGTCAGGCTTC 563  
 Oy 623 TTAAACAGAGCCTTCACTTATCTCTGACACGATTAATATGATTTAAACCTTTAAAC 682  
 Db 564 TTTCGACAGCCATCTTTTATCTGGAACCTTAT-----AAGTTTAAATTTTAAAG 619  
 Oy 683 CGCTTCACTGCTCCCACTGTGACCACTAAATGAACAATGTGTG 727  
 Db 620 CGATCTTACCTACTACTGCTGAAACCTCTAANGAACAATTCGGG 664

RESULT 6  
 BY735639 736 bp mRNA linear EST 17-DEC-2002  
 LOCUS BY735639 RIKEN full-length enriched, 1 cell embryo Mus musculus  
 DEFINITION cDNA clone 10C0031F16 5', mRNA sequence.  
 ACCESSION BY735639  
 VERSION BY735639.1 GI:271148766  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 736)  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojibori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.W., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brdic, D., Brusic, V., Chochua, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, J., Jarvis, E.D., Kana, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pereira, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Savelkin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Vetraro, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyszewski, B., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carlini, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, O., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, K., Shibata, K., Shinagawa, A., Yaumishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 MEDLINE 22354683  
 PUBMED 12468851  
 COMMENT Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Saitama-cho, Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carlini, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, O., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Osato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse libraries.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES  
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 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
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ORIGIN  
 Query Match 26.1%; Score 231.6; DB 6; Length 736;  
 Best Local Similarity 63.2%; Pred. No. 3.4e-46;  
 Matches 463; Conservative 0; Mismatches 242; Indels 28; Gaps 6;  
 Oy 86 GACCCGCTGCGGAGGACGACGAGCTGTGCGCCGACCTGAGCTGAGCGCCCG 145  
 Db 29 GACCCGCTGAGTGAAGACGACCTGAGCGCTGTGCTGCTGCTGCTGCTGCTGCTG 88  
 Oy 146 GAACCCGAGACCCCGGAGCCGCGCCATTCACGCGCCGAGCGCGCTGCTGCTGCG 205  
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 Oy 206 GCGCCGAGTGAAGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265  
 Db 149 ACTAGGAGATTCAGGAGGAGGACCAAGAAATTTTCTCTCTCTGCGAAGCGCGG 208  
 Oy 266 AACCGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325  
 Db 209 AATGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 268  
 Oy 326 ACTGCGGAGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 385  
 Db 269 AGCTGAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 328  
 Oy 386 CTGGTGAAGCGCCGCTGAGAGAGTGGGCTTTCAGACCGCGCTAAAGAGCAGAGGCG 445  
 Db 329 TACATGCTGTCAAGCAGAAAG-----GGGATCTGGGGATCGTGC 370



KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 758)  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Kathleen Horner, Stanford University  
CDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: NDAm1195 row: n column: 06  
High quality sequence stop: 623.  
Location/Qualifiers  
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/lab\_host="DH10B TONa"  
/clone\_1lb="NIH\_MGC\_256"  
/note="Organ: oocyte; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; cDNA was primed using oligo-dT primer: 5'-pGACTGTTCTAGATCGGACGGCGCCCTT)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.2 kb. This is a primary library (normalized primary library is NIH\_MGC\_257) and was constructed by Express Genomics (Frederick, MD).  
Note: this is a NIH\_MGC library"

ORIGIN

Query Match 24.9%; Score 220.8; DB 7; Length 758;  
Best Local Similarity 64.6%; Pred. No. 1.6e-43;  
Matches 371; Conservative 0; Mismatches 182; Indels 21; Gaps 2;

QY 86 GACCCGCTGCGGAGCGGACGAGCTGTTGCTGCGGACGCTGAGGCTACTGCGCCGG 145  
DB 51 GACCCGCTGCGGAGCGGACGAGCTGTTGCTGCGGACGCTGAGGCTACTGCGCCGG 110  
QY 146 GAACCCGAGACCCCGGAGCGGCGGACGAGCTGTTGCTGCGGACGCTGAGGCTACTGCGCCGG 205  
DB 111 GAGCCGAGACCCCGGAGCGGCGGACGAGCTGTTGCTGCGGACGCTGAGGCTACTGCGCCGG 170  
QY 206 GCCGCGAGTTACGCGGAGATTCACCGGCTCTTTTCTCCGCTACTGCGGCTACCCCGGG 265  
DB 171 ACTAGGAGATTCAGCGAGGACCAAGAAATTTTCTCTCTCTGGAAGCGCGGGCC 230  
QY 266 AACCGCTTCAAGCTGTGGCGGCTGATGCGGATTCGCTCTCTGCAAGCGCCGCGCC 325  
DB 231 AATCGCTGAGGCTGTGAAACAGATGACGATTAAGTTGCTCTCAAGACCAAGACTTC 290  
QY 326 ACCGCGGAGAGAGTGAGCGCTGTAAGCTTCCAGGAGAGCGCTGAGAGAGGCGCG 385  
DB 291 AGCTGGAGCAGAGTGATGATCTCTGCGCTTCCGGGAGCGCTTAATCAAGGCGCT 350  
QY 386 CTGGTGAACCGCCCGGTGAAGAGTGGGGCTTCCAGCGCGGCTAAAGAGCAGAGGCG 445  
DB 351 TACATGCTGTCAAGCAGAAAG-----GGATCTGGGAATCTGTCTC 392  
QY 446 GAGCTGCGCGGAGAGCTGCAAGCGCTGTGGCTTTGCTGAGCTCGCGCTCAGGCG 502  
DB 393 ATAGTGAACCGAGAGCTGCTCTCATAGTGAATCTTGTATTAATCTGCTCATGGGCGCT 452

QY 503 CAGCACCAGCGCTGCTGAGAGCTCAGGCGCGCTGAGATGCTTTGTCACTTCTCAGG 562  
DB 453 CGGACACCGCGGCTGAGAGCTCTGCGCGCTGAGATGCTTTGTCCGCTTTTCAAG 512  
QY 563 ACCCGCTTTCAGCTGCGCTTTTGGAGAAACAGCTGTCTCAGGCTTTTGTCAAGCTTG 622  
DB 513 AATCTTTCAGCTGCGCTTTTGGAGAAAGATGCTGATTCAGGCTTTTGTCAAGCTTG 572  
QY 623 TTACACAGCGCTTATTTATCTGAGACAGAT 656  
DB 573 TTGCAACAGCGCTTATTTATCTGAGAAAGCTT 606

RESULT 9  
LOCUS COB06531  
DEFINITION AGNCOURT 30256704 NIH\_MGC\_256 Mus musculus cDNA clone  
ACCESSION IMAGE:30938765 5', mRNA sequence.  
VERSION COB06531  
KEYWORDS COB06531.1 GI:51021322  
SOURCE EST.  
ORGANISM Mus musculus (house mouse)  
REFERENCE Mus musculus.  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Kathleen Horner, Stanford University  
CDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: NDAm1198 row: d column: 06  
High quality sequence start: 19  
High quality sequence stop: 527.  
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/db\_xref="taxon:10090"  
/clone="IMAGE:30938765"  
/lab\_host="DH10B TONa"  
/clone\_1lb="NIH\_MGC\_256"  
/note="Organ: oocyte; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; cDNA was primed using oligo-dT primer: 5'-pGACTGTTCTAGATCGGACGGCGCCCTT)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.2 kb. This is a primary library (normalized primary library is NIH\_MGC\_257) and was constructed by Express Genomics (Frederick, MD).  
Note: this is a NIH\_MGC library"

ORIGIN

Query Match 24.1%; Score 213.6; DB 7; Length 821;  
Best Local Similarity 61.3%; Pred. No. 9.7e-42;  
Matches 404; Conservative 0; Mismatches 229; Indels 26; Gaps 3;

QY 81 TGGCCGACCCGCTGCGGAGGAGCGAGCTGTTGCTGCGGACGCTGAGGCTACTGCGG 140  
DB 3 TGGCTTAAGACAGTTCGCGCGGAGATTCGCGGATGCTGTGACTACATATTTCTTGGCG 62  
QY 141 CCCGGAACCCCGGAGCCCGGAGCGCGCATTCAGCCCGAGGCGCGCGCTGCGCT 200  
DB 63 CAGCGAGCGGAGACCCGAGAGCGGCGCAGCTGCTGTGAGAGCGCGCTTGTGCTT 122

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Oy 201 CCGGCGCCGCGGAGTTACGGAGATTACCGGTCCTTTTCCTCCGCTACCTCGGCTACC 260
Db 123 CTGTGATCAGGAGATCCAGAGAGAGACCAAGATTTTTCCTTCCTTCGCGAAACCC 182
Oy 261 CCGGAGACCGCTTCAGCTGTGTGGCGGTGATGGCGGATTCGGTCTTCCTCCGACACGCCCG 320
Db 183 GGGGCAATCGCTGTGAGCTGGTGAACAAGATGGCAGATAGTTGCTCTCCAAAGACCAAG 242
Oy 321 GCCCAGCTGGGGCAGATGTGAGCTCGTACCTTTGGCAGGACCGTGTGCTGGAGAG 380
Db 243 ACTTGAAGTGAAGCAACTGGATGATCTTCGGCTTCGGCGGAGACGCTTATGAATCAAG 302
Oy 381 GAGCGCTGGTGAACCGCCGCTGAGAGAGATGGGGCTTCACGCGCGGCTAAAGAGCAGG 440
Db 303 GCCCTTACATGCTGTCTCAAGCAGAGA-----GGGATCTGGGGAATC 344
Oy 441 AGGGCAGCTGCGCCCGGAGACTGCGACGCGCTGTGGCTGTGAGCTCGCGGCTCATGG 500
Db 345 GTGTCAATAGTACCCGAGACTGCTGTCTCATAGTGAATCTTGTATATCTGCTCATGG 404
Oy 501 GG----CAGCAGCGCGCTGCGCTGCGAGGCTCAGAGGCGGCTGGAGATGGCTTTGTCTCT 557
Db 405 GAGCGTGGCAGCGCGCAGGCTGAGGCTCTCGCGGCTGGAGTGGCTTTTGGCGCTTCT 464
Oy 558 TCAGAGACCCCTTTTCAGCTGCTTTTGGAGAGAAACAGCTGGTCAGGCTTTTCTGTAT 617
Db 465 TCAGAAATCTTTACCGCTCGCTCGCTTCGAGAGAAATGCTGATTCAGGCTTTTCTGTAG 524
Oy 618 GCTTGTAAACAACAGCTTTCATTATCTCTGGACAGATTAATATAGTTTAAACTTT 677
Db 525 GCTTCTTTTGGACAGCCCATCTTTTATCTGGNAAACCTTATTA-----GTTTAAATTT 579
Oy 678 TAAACCCGCTTACCTGCGCAACTGTGACCAACTAATAGACAGATGTGGAGAACAA 736
Db 580 TAAAGCGATCTTACTTACTTACTGTGAACCTCTAAGAGAACATTTCTGGATNTNNA 638
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RESULT 10
LOCUS CA560564 524 bp mRNA linear EST 19-NOV-2002
DEFINITION K0274C06-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
ACCESSION CA560564
VERSION CA560564.1 GI:25105219
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 524)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Steggy, C.A.,
Martin, P., Abda, K., Tanaka, T. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
(Long)
Unpublished (2001)
Other ESTs: K0274C06-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0274 row: C column: 06
Seq primer: M13 Reverse
High quality sequence stop: 524
POLYA=No.
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FEATURES

Source

1..524

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="naest:K0274C06-5N"

/db\_xref="taxon:10090"

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/clone="NIA:K0274C06 IMAGE:30051773"
/feature="unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library
(Long)"
/vector="pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igsun.grc.nia.nih.gov/cdna). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen):
5'-TGACTAGTCTAGATCGGAGCGGCGCCCTTTTCTTTTCTTTT-3',
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-Linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NIA)."
```

## ORIGIN

Query Match 23.3%; Score 206.4; DB 6; Length 524;  
Best Local Similarity 64.6%; Pred. No. 5.3e-40;  
Matches 350; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

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Oy 116 CTGCGCCACTACCTGGGGTACTGGCCCGGAGACCCCGGAGCCCGGCGCCATCC 175
Db 1 CTGTCTGACTAATATTTCTTCTGCGCGGGAGCGGACACCCAGAGCCACCGCCACG 60
Oy 176 ACGCCGAGCGCGCGCTGCTCGCGCGCCGCGGAGTTACGAGATTCACCGGTCC 235
Db 61 TCTGTGAGCGCGCTTCTGCTGTGTATGAGGAGATCCAGCAGACACCAAGAA 120
Oy 236 TTTTTCCTCGCTACCTGCGTACCCCGGAGACGCTTTCAGCTGTGGCCGCTAATGGCG 295
Db 121 TTTTTCCTCTCTCTCGGAAAGCCGGGGCAATGCGCTGAGCTGTGTAACAATATGCA 180
Oy 296 GATTCGCTCTCTCCAGACGCGCGCCGCTGCGGCGAGAGTGTGACCTGTGACC 355
Db 181 GATTAAGTGTCTCTCAAGACCAAGACTTCAGCTGAGCCAACTGTGATGCTCTTGACC 240
Oy 356 TTGCGAGGAGCGCTGTGAGAGAGCGCGCTGTGACCGCCCGGTGGAAGATGGGGC 415
Db 241 TTGCGGAGAGCGCTTATGAAATCAAGCCCTTACATGCTGTGCAAGCAGAGAA----- 292
Oy 241 TTGCGGAGAGCGCTTATGAAATCAAGCCCTTACATGCTGTGCAAGCAGAGAA----- 292
Oy 416 TTCAGCGCGGCTAAAGAGAGAGGCGACGCTGCGCGGAGACTGCGCAGCGCTGTG 475
Db 293 -----GGGATCTGGGGAATCGTGTCTAATGTGACCCGAGACTGCTGTCTATAGTG 342
Oy 476 GCTTGTGAGCTGCGCGCTCATAGGG-----CAGACCGCGCGCTGCGCAGGCTCAGGG 532
Db 343 AACTTCTGTATTAATGTGCTATGAGGCGGTGGACCGCGCAGGCTGAGAGCTTCTGCGC 402
Oy 533 GAGTGGAGATGCTTTTGTGCACTTCTTGAAGACCCCTTTCACATGAGCTTTTGGAGAAA 592
Db 403 GAGTGGAGATGCTTTTGTGCGCTTCTTCAAGAAATCTTACAGCTGCGCTTCTGAGAGAA 462
Oy 593 CAGTGTGTCAGGCTTTTGTGCAATGCTTGAACAACAGCTTCAATTAATCTTGACA 652
Db 463 TTGCTGATTCAGGCTTTTCTGTACAGCTTCTTGAACAGACATCTTTTATCTGGAAA 522
Oy 653 CG 654
Db 523 CG 524
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RESULT 11  
 LOCUS COB08612 763 bp mRNA linear EST 06-AUG-2004  
 DEFINITION AGNCOURT 30256728 NIH MGC 256 Mus musculus cDNA clone  
 IMAGE:30938958 5', mRNA sequence.  
 COB08612  
 ACCESSION COB08612  
 VERSION GI:51025466  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 763)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cga9bs-remail.nih.gov  
 Tissue Procurement: Dr. Kathleen Horner, Stanford University  
 cDNA Library Preparation: Express Genomics  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNI)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ULNI at:  
 http://image.llnl.gov  
 Plate: NDAM198 row: 1 column: 07  
 High quality sequence stop: 540.  
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 /lab\_host="DH10B TONa"  
 /clone\_lib="NIH\_MGC\_256"  
 /note="Organ: oocyte; Vector: pExpress-1; Site 1: EcoRV;  
 Site 2: NotI; cDNA was primed using oligo-dT primer:  
 5'-pGAGTGTCTAGATCGGAGCGGCGCC(T)25-3' and cloned into  
 the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb  
 resulted in an average insert size of 1.2 kb. This is a  
 primary library (normalized primary library is NIH\_MGC\_257)  
 and was constructed by Express Genomics (Frederick, MD).  
 Note: this is a NIH\_MGC library"

Query Match 21.6%; Score 191.6; DB 7; Length 763;  
 Best Local Similarity 63.8%; Pred. No. 2.6e-36;  
 Matches 351; Conservative 0; Mismatches 174; Indels 25; Gaps 3;

181 CGAGGCGCGGTCGCGGCTCCGCGCGCCGACGATTACGCGGCTCTTTT 240  
 Db 11 CGAGCGCGCTTCTTCTCTCTGATGACGAGATCCAGCGAGACCAAGAAATTTT 70  
 Qy 241 CTCGCGCTACCTCGGCTACCCCGGGAACCGCTTCAGCTGTGTGGCTGATGGCGGATTC 300  
 Db 71 TTCCTCTTTCGGAAGACCGGGGCAATCGCTGAGCTGGTGAAGACAGATGGAGATTA 130  
 Qy 301 CGTGTCTTCGACAGACCCCGGCGCCCACTGGGGCAGAGTGTGACGCTCTGTAACCTTGGC 360  
 Db 131 GTTGTCTTCCAAAGACCAAGACTTCAGCTGGAGCCAACTGTGTGATCTCTGGCCCTTGC 190  
 Qy 361 AGGAGCGTGTGAGAGAGGCGCGCTGTGACCGCGCGGTGAGAGAGTGGCGCTTCA 420  
 Db 191 GGGAGCGCTTAAATCAAGGCTTTACATGGCTTCAAGAGAA----- 237  
 Qy 421 GCCGCGCTAAAGAGAGAGGCGAGCGTCCCGGAGACTGCCAGCGCTGTGGCTT 480  
 Db 238 -----GGGATCTGGGGAATCGTGTATAGTACCCGAGACTGCTGTCTCATAGTAACCTT 292

Qy 481 GGTGAGCTCGGCGCTCATGGG---CAGCAGCGGCGCTGGCTGAGGCTCAGGCGGCTG 537  
 Db 293 TCTGATATATCTGCTCAAGGCGCGTGGCAGCGGCGCCAGGCTGTGAGGCTCTCGGCGGCTG 352  
 Qy 538 GGATGCTTTTGTGCACTTCTTCAAGACCCCTTTCACATGCTTTTGGAGAAAACAGCT 597  
 Db 353 GGATGCTTTTGGCGGCTTCTTCAAGAACTCTTACCGCTCGGCTTCTGGAGAAATGCT 412  
 Qy 598 GGTCCAGGCTTTTGTGTATGCTGTGTAACAACAGCTTCAATTATCTGTGACAGATT 657  
 Db 413 GATTGAGGCTTTTGTGTATGCTGTGTAACAACAGCTTCTTTTATCTGGAACGTTT 472  
 Qy 658 ATTATGAGTTTAAACCTTTAAACCGCTTACCGCCCAAGCTGACCAACTAAATGA 717  
 Db 473 AT---AGTTTAAATTTTAAAGCGATCTTACTTACTTACTGTAACCTCTTAAGGA 528  
 Qy 718 CAGATGTGTG 727  
 Db 529 ACATTCTGG 538

RESULT 12  
 LOCUS AA005293 206 bp mRNA linear EST 07-MAY-1997  
 DEFINITION zhs3all.r1 Soares fetal liver spleen INFLS\_S1 Homo sapiens cDNA  
 clone IMAGE:428828 5', mRNA sequence.  
 AA005293  
 ACCESSION AA005293  
 VERSION AA005293.1 GI:1448755  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 206)  
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
 Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, N.,  
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
 Rohlfing, T., Scheinberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
 Trevaekis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.  
 and Marra, M.  
 TITLE Genomewide and analysis of 280,000 human expressed sequence tags  
 JOURNAL 97044478  
 MEDLINE 8889549  
 PUBMED  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1810  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 849 Std Error: 0.00  
 Seq primer: mob.REGA+RF  
 High quality sequence stop: 126.  
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 /db\_xref="GDB:1328597"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:428828"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_fetal\_liver\_spleen\_INFLS\_S1"  
 /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)  
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
 This is a subcloned version of the original Soares fetal  
 liver spleen INFLS library. 1st strand cDNA was primed  
 with a Pac I - oligo(dT) primer [5'



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 893)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgap@nci.nih.gov](mailto:cgap@nci.nih.gov)  
Tissue Procurement: Dr. Kathleen Horner, Stanford University  
CDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: NDAMI19 row: n column: 14  
High quality sequence stop: 538.  
Location/Qualifiers

FEATURES  
source

1. 893  
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/clone="IMAGE:30939397"  
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/note="Organ: oocyte; Vector: pExpress-1; Site: 1: EcoRV,  
Site 2: NotI; CDNA was primed using oligo-dT primers:  
5'-pGACTAGTTCTGATCGGAGCGCCGCTT(25-3' and cloned into  
the EcoRV/NotI sites of pExpress-1. Size selection >0.5 kb  
resulted in an average insert size of 1.2 kb. This is a  
primary library (normalized primary library is NIH\_MGC\_257)  
and was constructed by Express Genomics (Frederick, MD).  
Note: this is a NIH\_MGC library"

## ORIGIN

Query Match 19.1%; Score 169.8; DB 7; Length 893;  
Best Local Similarity 61.6%; Pred. No. 6.4e-31;  
Matches 317; Conservative 0; Mismatches 177; Indels 21; Gaps 2;

86 GACCCGCTGCGGAGACCGCAGCTGTTGCTGCGCAGTACTAGGAGTCTGCGCCG 145  
|||  
168 GACCCATGATGATGAGACGACGCTGCTGTGATCATATTTCTTCTGCGCAGC 227  
|||  
146 GAACCCGACCCCGAGCGCGCATCAACGCCGAGCGCGCTGCGCTCGCGC 205  
|||  
228 GAGCCGACACCCGAGACCGCCCACTGTGTGAGGCGCGCTTCTGCTGTG 287  
|||  
206 GCCCGCAGTTCAGGCGATTCACCGCTTTTTCGCCGCTACCTCGGCTACCCGCG 265  
|||  
288 ACTAGGAGATTCAGGAGACCGACCAAGATTTTCTCTTCTGTGAAAGCGCGGC 347  
|||  
266 AACCGTTTCAGCTGTGCGCTGATGCGGATTCGCTCTCCGACAGCCCGCCG 325  
|||  
348 AATGCGCTGAGCTGTGTGAACAATGCGATTAAGTTCTCTCCAAAGACCAAGACTTC 407  
|||  
326 ACTGCGGCAAGATGTGACGCTGTGACCTTTCGAGGAGCGTGTGAGAGAGGCGC 385  
|||  
408 AGCTGAGACCAATGTGTATGCTCTGCGCGGAGACGTTATTAATCAAGGCCCT 467  
|||  
386 CTGTGACCGCCCGGTGAAGAGATGGGGCTTCCAGCGCGGCTTAAGAGACAGAGGC 445  
|||  
468 TACATGCTGTCAAGACAGAA-----GGATCTGGGGAATCTGTCTC 509  
|||  
446 GACCTGCGCGGAGCTGCGCAGCGCTGTGCTTGTGAGCTGCGCGCTCATGGG--- 502  
|||  
510 ATAGTACCGAGACTGTCTCTCATATGAACTTTCTGTATTAATCTGCTCATGGGCGT 569  
|||  
503 CAGACCGCGCTGTGCTGAGGCTCAAGGCGCGCTGGAGATGAGCTTTTGTCACTTTCCAG 562  
|||  
570 CGGACCGCGCGAGGCTGTGTCTGTGCGCGCTGTGAGATGCTTTTGTGCGCTTCTTCA 629  
|||

Qy 563 ACCCCCTTTCACATGCTTTTGGAGAAACAGCT 597  
|||  
Db 630 ATCTTTACCGCTCGCTTCTGAGAAATGCTGAT 664  
|||

RESULT 15  
BX119239/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BX119239 535 bp mRNA linear EST 10-FEB-2003  
BX119239 Soares infant brain INIB Homo sapiens cDNA clone  
IMAGE988N01170 ; IMAGE:40052, mRNA sequence.  
BX119239  
BX119239.1 GI:27841652  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 535)  
Ebert, L., Hell, O., Hennig, S., Neubert, P., Patsch, E., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished (2003)  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD: IMAGE988N01170.  
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
<http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972> Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)

FEATURES  
source

Location/Qualifiers

1. 535  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE988N01170 ; IMAGE:40052"  
/sex="female"  
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/lab\_host="MDH10B (ampicillin resistant)"  
/clone\_lib="Soares infant brain INIB"  
/note="Organ: whole brain; Vector: LaFmid BA; Site 1: Not  
I; Site 2: Hind III; 1st strand cDNA was primed with a Not  
I - oligo(dT) primer (5'  
AATGTAAGAAATTCGCGCGCGAGAAATTTTTTTTTTTTTTTT 3');  
double-stranded cDNA was ligated to Hind III adaptors  
(Pharmacia), digested with Not I and directionally cloned  
into the Not I and Hind III sites of the LaFmid BA vector.  
Library went through one round of normalization. Library  
constructed by Bento Soares and M.Felicia Bonaldo."

## ORIGIN

Query Match 18.8%; Score 167; DB 5; Length 535;  
Best Local Similarity 100.0%; Pred. No. 2.9e-30;  
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

721 ATGTGTAGAAACAAAGCTAGAGGAACCTTCCCAACCCAGAGCTTTTATCTGA 780  
|||  
Db 535 ATGTGTAGAAACAAAGCTAGAGGAACCTTCCCAACCCAGAGCTTTTATCTGA 476  
|||  
Qy 781 ATGATACAAAGAGTCTGAGAGTGTGATTTGGCAATGTTTAACTTGTGAAGAAGT 840  
|||  
Db 475 ATGATACAAAGAGTCTGAGAGTGTGATTTGGCAATGTTTAACTTGTGAAGAAGT 416  
|||  
Qy 841 CAGGTGAGGACAAAGATCAATGCTCTTCTTGTAGTAAAGAA 887  
|||

Wed Jun 8 10:19:30 2005

us-10-071-174a-1.rst

Page 12

Db 415 CAGGTGTGAGGACAGAAATGCGCTTCTTGAGTGAAAGAA 369

Search completed: June 7, 2005, 17:48:10  
Job time : 5400.65 secs

9

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2005, 08:53:39 ; Search time 1000.5 Seconds  
(without alignment)  
6296.021 Million cell updates/sec

Title: US-10-071-174A-37  
Perfect score: 130  
Sequence: 1 tccgcctaccctcgagctacc.....accttcgagggagcgcgcgt 130

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114.8	88.3	582	6	BD233456 Human pro
2	114.8	88.3	582	6	HS458330 Homo sapi
3	114.8	88.3	615	9	AF285092 Homo sapi
4	114.8	88.3	726	6	CQ752105 Sequence
5	114.8	88.3	887	9	AF326964 Homo sapi
6	114.8	88.3	1168	6	BD233466 Homo sapi
7	114.8	88.3	93287	9	AC023906 Homo sapi
8	88.8	68.3	214669	2	AC018903 Homo sapi
9	55.4	42.6	1074	10	AY029163 Rattus no
10	55.4	42.6	240461	2	AC111659 Rattus no
11	51	39.2	1209	10	AF102501 Mus muscu
12	51	39.2	1225	10	AF067660 Mus muscu
13	51	39.2	1257	10	BC052690 Mus muscu
14	51	39.2	168997	10	AC133947 Mus muscu
15	51	39.2	202851	10	AC115880 Mus muscu
16	37	28.3	3389	1	SAGLCTRAA
17	36.8	28.3	3288	6	AR034064 Sequence
18	36.8	28.3	3288	6	AR097654 Sequence
19	36.8	28.3	3288	6	AR097731 Sequence

c	20	36.8	28.3	3288	6	AR102358 Sequence
c	21	36.8	28.3	3288	6	AR104868 Sequence
c	22	36.8	28.3	3288	6	AR131079 Sequence
c	23	36.8	28.3	3288	6	AR137601 Sequence
c	24	36.8	28.3	3288	6	AR453135 Sequence
c	25	36.8	28.3	3288	6	BD023245 Method fo
c	26	36.8	28.3	3288	10	MMUJ31993 Mus musculu
c	27	36.8	28.3	111775	10	AC018559 Mus muscu
c	28	36.8	28.3	152316	10	AC007844 Mus muscu
c	29	36.8	28.3	170323	10	AC078896 Mus muscu
c	30	36.8	28.3	209282	10	AC135105 Mus muscu
c	31	36.2	27.8	142121	9	AC036103 Homo sapi
c	32	36.2	27.8	145631	2	AC087460 Homo sapi
c	33	36.2	27.8	173660	9	AC084693 Homo sapi
c	34	36.2	27.8	175137	2	AC018670 Homo sapi
c	35	36.2	27.8	187872	2	AC067988 Homo sapi
c	36	36	27.7	301675	1	AP005027 Streptomy
c	37	35.4	27.2	868	5	CR523779 Gallus ga
c	38	35.4	27.2	1291	8	AK106045 Oryza sat
c	39	35.4	27.2	1724	6	BD016979 Starch sy
c	40	35.4	27.2	2412	6	AK755428 Oryza sat
c	41	35.4	27.2	2919	8	AK101978 Oryza sat
c	42	35.4	27.2	2959	8	AF419099 Oryza sat
c	43	35.4	27.2	4422	8	AY423717 Oryza sat
c	44	35.4	27.2	151668	8	AP003509 Oryza sat
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#### ALIGNMENTS

RESULT 1	BD233456	582 bp	DNA	linear	PAT 17-JUN-2003
LOCUS	BD233456				
DEFINITION	Human protein having hydrophobic domain and DNA encoding the same.				
ACCESSION	BD233456.1	GI:33043226			
VERSION	BD233456.1				
KEYWORDS	JP 2002519016-A/2.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Kato, S. and Kimura, T.				
TITLE	Human protein having hydrophobic domain and DNA encoding the same				
JOURNAL	Patent: JP 2002519016-A 2 02-JUN-2002;				
COMMENT	SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC				
OS	Homo sapiens (human)				
PN	JP 2002519016-A/2				
PD	02-JUN-2002				
PF	18-JUN-1999	JP 2000557267			
PI	SEISHI KATO,TOMOKO KIMURA				
PC	C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N5/10,C12N15/00,C12N5/PC				
CC	Human protein having hydrophobic domain and DNA encoding the				
CC	same				
FT	Key	Location/Qualifiers			
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ORIGIN	Query Match	88.3%	Score 114.8 ;	DB 6 ;	Length 582 ;
	Best Local Similarity	96.9%	Pred. No. 1.7e-15 ;		
	Matches 127 ;	Conservative 0 ;	Mismatches 3 ;	Indels 1 ;	Gaps 1 ;
QY	1	TCCGCTTACCTCGACTACCCCGGACCGCTTCGAGCTGTCGCTGATGCGCATTC	60		

Db 163 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 222  
QY 61 GTGCTCTCGACAGCCCGGACCTT-GGGAGNAGTGTGACGCTGTGACCTTGC 119  
Db 223 GTGCTCTCGACAGCCCGGACCTTGGGACAGTGTGACGCTGTGACCTTGC 282  
QY 120 GGGAGCTGCT 130  
Db 283 GGGAGCTGCT 293

RESULT 2  
HSA458330 585 bp DNA linear PRI 25-APR-2002  
LOCUS Homo sapiens NRH gene for anti-apoptotic protein.  
DEFINITION AJ458330  
ACCESSION AJ458330.1 GI:20338765  
VERSION anti-apoptotic protein; NRH gene.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Anouachetia, A., Arnaud, E., Venet, S., Lalle, P., Gony, M., Rigal, D. and  
Gillet, G.  
TITLE Nr1p, a human homologue of Nr-13 associates with Bcl-Xs and is an  
inhibitor of apoptosis  
JOURNAL Oncogene 20 (41), 5846-5855 (2001)  
MEDLINE 21477277  
PUBMED 11593390  
REFERENCE 2 (bases 1 to 585)  
AUTHORS Gillet, G.  
TITLE Direct Submission  
JOURNAL Submitted (23-APR-2002) Gillet G., IDCP, CNRS UMR 5086, 7 PASSAGE  
DU VERORS, 69367, FRANCE

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location/Qualifiers  
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ORIGIN  
Query Match 88.3%; Score 114.8; DB 9; Length 585;  
Best Local Similarity 96.9%; Pred. No. 1.7e-15;  
Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Db 1 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 60  
QY 163 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 222  
QY 61 GTGCTCTCGACAGCCCGGACCTT-GGGAGNAGTGTGACGCTGTGACCTTGC 119  
Db 223 GTGCTCTCGACAGCCCGGACCTTGGGACAGTGTGACGCTGTGACCTTGC 282  
QY 120 GGGAGCTGCT 130  
Db 283 GGGAGCTGCT 293

RESULT 3  
AF285092 615 bp mRNA linear PRI 08-NOV-2001  
LOCUS Homo sapiens Bcl-2-like protein 10 mRNA, complete cds.  
DEFINITION AF285092  
ACCESSION AF285092  
VERSION AF285092.1 GI:9837265  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Zhang, H., Holzgreve, W., and De Geyter, C.  
TITLE Bcl2-L-10, a novel anti-apoptotic member of the Bcl-2 family,  
blocks apoptosis in the mitochondria death pathway but not in the  
death receptor pathway  
JOURNAL Hum. Mol. Genet. 10 (21), 2329-2339 (2001)  
MEDLINE 21548034  
PUBMED 11689480  
REFERENCE 2 (bases 1 to 615)  
AUTHORS Zhang, H.H.  
TITLE Direct Submission  
JOURNAL Submitted (05-JUL-2000) University Women's Hospital, Schanzenstr  
46, Basel 4057, Switzerland

FEATURES  
source  
location/Qualifiers  
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/map="15q21"  
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/db\_xref="GI:9837266"  
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RLRQTHRSFSAHYIGYGNRRELVAMADSVLSRPGTWGVTVLVTFAGTLERGP  
LVTAIRKRWGQPRLEKQBGVARDQRLVALLSRRLMGHRAMLQAGGWDGFCHEP  
RTPPLAFWRKQLVQAFLSCLTTAFIYLTREL"

ORIGIN  
Query Match 88.3%; Score 114.8; DB 9; Length 615;  
Best Local Similarity 96.9%; Pred. No. 1.7e-15;  
Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 60  
Db 193 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 252  
QY 61 GTGCTCTCGACAGCCCGGACCTT-GGGAGNAGTGTGACGCTGTGACCTTGC 119  
Db 253 GTGCTCTCGACAGCCCGGACCTTGGGACAGTGTGACGCTGTGACCTTGC 312  
QY 120 GGGAGCTGCT 130  
Db 313 GGGAGCTGCT 323

RESULT 4  
CO752105 726 bp DNA linear PAT 03-FEB-2004  
LOCUS Sequence 38039 from Patent W002068579.  
DEFINITION CO752105  
ACCESSION CO752105.1 GI:42387450  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof  
JOURNAL Patent: WO 02068579-A 38039 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES location/Qualifiers  
source 1..726  
/organism="Homo sapiens"  
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ORIGIN  
Query Match 88.3%; Score 114.8; DB 6; Length 726;  
Best Local Similarity 96.9%; Pred. No. 1.6e-15;  
Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGGATTC 60  
Db 193 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGGATTC 252

Qy 61 GTGCTCTCCGACAGCCCGGCGCCCACT-GGAGNAGTGTGACGCTGTGACCTTGCA 119  
Db 253 GTGCTCTCCGACAGCCCGGCGCCCACTGTGGGAGAGTGTGACGCTGTGACCTTGCA 312

Qy 120 GGGACGCTGCT 130  
Db 313 GGGACGCTGCT 323

RESULT 5  
AF326964  
LOCUS AF326964 887 bp mRNA linear PRI 01-MAY-2001  
DEFINITION Homo sapiens BCLB (BCLB) mRNA, complete cds.  
ACCESSION AF326964  
VERSION AF326964.1 GI:13898393  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 887)  
AUTHORS Ke,N., Godzik,A. and Reed,J.C.  
TITLE Bcl-B, a novel Bcl-2 family member that differentially binds and regulates Bax and Bak  
JOURNAL J. Biol. Chem. 276 (16), 12481-12484 (2001)  
MEDLINE 21201065  
PUBMED 11278245  
REFERENCE 2 (bases 1 to 887)  
AUTHORS Ke,N., Godzik,A. and Reed,J.C.  
TITLE Direct Submission  
JOURNAL Submitted (07-DEC-2000) The Burnham Institute, 10901 N. Torrey Pines Rd., La Jolla, CA 92037, USA  
FEATURES location/Qualifiers  
source 1..887  
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ORIGIN GSWDFGHFRTPEPLAFMRKOLVOAFLSCLTTAFIYLTWRLR"

Query Match 88.3%; Score 114.8; DB 9; Length 887;  
Best Local Similarity 96.9%; Pred. No. 1.6e-15;  
Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGGATTC 60  
Db 242 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGGATTC 301

Qy 61 GTGCTCTCCGACAGCCCGGCGCCCACT-GGAGNAGTGTGACGCTGTGACCTTGCA 119  
Db 302 GTGCTCTCCGACAGCCCGGCGCCCACTGTGGGAGAGTGTGACGCTGTGACCTTGCA 361

Qy 120 GGGACGCTGCT 130  
Db 362 GGGACGCTGCT 372

RESULT 6  
BD233466  
LOCUS BD233466 1168 bp DNA linear PAT 17-JUL-2003  
DEFINITION Human protein having hydrophobic domain and DNA encoding the same.  
ACCESSION BD233466  
VERSION BD233466.1 GI:33043236  
KEYWORDS JP 2002519016-A/12.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1168)  
AUTHORS Kato,S. and Kimura,T.  
TITLE Human protein having hydrophobic domain and DNA encoding the same  
JOURNAL Patent: JP 2002519016-A 12 02-JUL-2002;  
COMMENT SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC  
OS Homo sapiens (human)  
PN JP 2002519016-A/12  
PD 02-JUL-2002  
PF 18-JUN-1999 JP 2000557267  
PI SEISHI KATO,TOMOKO KIMURA  
PC C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N5/10,C12N15/00,C12N5/PC 00

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FH Key same  
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FT location/Qualifiers  
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/db\_xref="taxon:9606"

ORIGIN

Query Match 88.3%; Score 114.8; DB 6; Length 1168;  
Best Local Similarity 96.9%; Pred. No. 1.5e-15;  
Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGGATTC 60  
Db 169 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGGCGGATTC 228

Qy 61 GTGCTCTCCGACAGCCCGGCGCCCACT-GGAGNAGTGTGACGCTGTGACCTTGCA 119  
Db 229 GTGCTCTCCGACAGCCCGGCGCCCACTGTGGGAGAGTGTGACGCTGTGACCTTGCA 288

Qy 120 GGGACGCTGCT 130  
Db 289 GGGACGCTGCT 299

RESULT 7  
AC023906/c 93287 bp DNA linear PRI 06-JUN-2001  
LOCUS Homo sapiens chromosome 15 clone CTD-2184D3 map 15q21.2, complete  
DEFINITION sequence.  
ACCESSION AC023906  
VERSION AC023906.7 GI:14595770  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 93287)  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 93287)  
AUTHORS Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.  
TITLE Sequencing of human chromosome 15 D15S146-D15S117 region  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 93287)  
AUTHORS Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T., and Hood, L.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA  
REFERENCE 3 (bases 1 to 93287)  
AUTHORS Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.  
TITLE Direct Submission  
JOURNAL Submitted (04-JUN-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA  
REFERENCE 4 (bases 1 to 93287)  
AUTHORS Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA  
COMMENT On Jul 4, 2001 this sequence version replaced gi:12248292.  
----- Genome Center  
Center: Multimegabase Sequencing Center  
Center code: UMWSC  
Web site: http://chroma.mbt.washington.edu/msg\_www  
Contact: leerowen@systemsbiology.org  
----- Summary Statistics  
Sequencing vector: pUC18; L08752  
Chemistry: Dye-terminator Big Dye; 90% of reads  
Chemistry: Dye-primer Big Dye; 10% of reads  
Assembly program: Phrap; version 0.990399  
Note: Data from overlapping BACs AC010674 [drafting center: UMWSC], AC090970 [drafting center: UMWSC], and AC016824 [drafting center: GTC] was added for finishing  
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/db\_xref="taxon:9606"  
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/clone\_lib="Cal Tech Human BAC library D"  
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1. 8893  
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misc\_feature 1. 8893  
/note="Overlap with RP11-47K1 AC016824"  
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unure 14722. 14808  
/note="low quality data"  
unure 37627  
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/note="low quality data"  
misc\_feature 82012. 93287  
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Best Local Similarity 96.9%; Pred. No. 7.3e-16;  
Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 TCCGCTACCTCGGCTACCCCGGGAACGCTTCGAGTGTGGCGCTGATGCGGATTC 60  
Db 64750 TCCGCTACCTCGGCTACCCCGGGAACGCTTCGAGTGTGGCGCTGATGCGGATTC 64691  
Qy 61 GTGCTTCGACAGCCCCCGCCACCT-GGAGNAGTGATGAGCTTCGACCTTCGCA 119  
Db 64690 GTGCTTCGACAGCCCCCGCCACCTGGGGGAGAGTGTGAGCGTTCGACCTTCGCA 64631  
Qy 120 GGGAGCGTCTCT 130  
Db 64630 GGGAGCGTCTCT 64620  
RESULT 8  
AC018903 214669 bp DNA linear HTG 04-JUN-2000  
LOCUS Homo sapiens chromosome 15 clone RP11-337B11 map 15q21, LOW-PASS  
DEFINITION SEQUENCE SAMPLING.  
ACCESSION AC018903  
VERSION AC018903.2 GI:8247797  
KEYWORDS HTG; HTGS\_PHASEO.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 214669)  
AUTHORS Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Shaffer, T., and Hood, L.  
TITLE Sequencing of human chromosome 15 D15S146-D15S117 region  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 214669)  
AUTHORS Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Shaffer, T., and Hood, L.  
TITLE Direct Submission  
JOURNAL Submitted (22-DEC-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA  
COMMENT On Jun 4, 2000 this sequence version replaced gi:6630517.  
----- Genome Center  
Center: Multimegabase Sequencing Center  
Center code: UMWSC  
Web site: http://chroma.mbt.washington.edu/msg\_www  
Contact: leerowen@systemsbiology.org  
----- Summary Statistics  
Sequencing vector: pUC18; L08752  
Chemistry: Dye-terminator Big Dye; 90% of reads  
Chemistry: Dye-primer Big Dye; 10% of reads  
Assembly program: Phrap; version 0.990399  
\* NOTE: This record contains 192 individual  
\* sequencing reads that have not been assembled into

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* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
* 806: contig of 806 bp in length
* 807
* 906: gap of unknown length
* 907
* 2068: contig of 1162 bp in length
* 2069
* 2168: gap of unknown length
* 2169
* 3020: contig of 852 bp in length
* 3021
* 3120: gap of unknown length
* 3121
* 4284: contig of 1164 bp in length
* 4285
* 4384: gap of unknown length
* 4385
* 5201: contig of 817 bp in length
* 5202
* 5301: gap of unknown length
* 5302
* 6544: contig of 1243 bp in length
* 6545
* 6644: gap of unknown length
* 7472: contig of 828 bp in length
* 7473
* 7572: gap of unknown length
* 7573
* 8756: contig of 1184 bp in length
* 8757
* 8856: gap of unknown length
* 8857
* 9658: contig of 802 bp in length
* 9659
* 9758: gap of unknown length
* 9759
* 10905: contig of 1147 bp in length
* 10906
* 11005: gap of unknown length
* 11006
* 11811: contig of 806 bp in length
* 11812
* 11911: gap of unknown length
* 11912
* 13293: contig of 1382 bp in length
* 13294
* 13393: gap of unknown length
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* 14211: contig of 818 bp in length
* 14212
* 14311: gap of unknown length
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* 15465: contig of 1154 bp in length
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* 15565: gap of unknown length
* 15566
* 16379: contig of 814 bp in length
* 16380
* 16479: gap of unknown length
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* 17624: contig of 1145 bp in length
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* 17724: gap of unknown length
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* 18578: contig of 854 bp in length
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* 18678: gap of unknown length
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* 19774: contig of 1096 bp in length
* 19775
* 19874: gap of unknown length
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* 20700: contig of 826 bp in length
* 20701
* 20800: gap of unknown length
* 20801
* 22036: contig of 1236 bp in length
* 22037
* 22136: gap of unknown length
* 22137
* 23023: contig of 887 bp in length
* 23024
* 23123: gap of unknown length
* 23124
* 24196: contig of 1073 bp in length
* 24197
* 24296: gap of unknown length
* 24297
* 25141: contig of 845 bp in length
* 25142
* 25241: gap of unknown length
* 25242
* 26385: contig of 1144 bp in length
* 26386
* 26485: gap of unknown length
* 26486
* 27325: contig of 840 bp in length
* 27326
* 27425: gap of unknown length
* 27426
* 28691: contig of 1266 bp in length
* 28692
* 28791: gap of unknown length
* 28792
* 29655: contig of 864 bp in length
* 29656
* 29755: gap of unknown length
* 29756
* 30881: contig of 1126 bp in length
* 30882
* 30981: gap of unknown length
* 30982
* 31813: contig of 832 bp in length
* 31814
* 31913: gap of unknown length
* 31914
* 33056: contig of 1143 bp in length
* 33057
* 33156: gap of unknown length
* 33157
* 34007: contig of 851 bp in length
* 34008
* 35320: contig of 1213 bp in length
* 35321
* 35420: gap of unknown length
35421
* 36207: contig of 787 bp in length
* 36208
* 36307: gap of unknown length
* 36308
* 37521: contig of 1214 bp in length
* 37522
* 37621: gap of unknown length
* 37622
* 38420: contig of 799 bp in length
* 38421
* 38520: gap of unknown length
* 38521
* 39726: contig of 1206 bp in length
* 39727
* 39826: gap of unknown length
* 39827
* 40635: contig of 809 bp in length
* 40636
* 40735: gap of unknown length
* 40736
* 41845: contig of 1110 bp in length
* 41846
* 41945: gap of unknown length
* 41946
* 42730: contig of 785 bp in length
* 42731
* 42830: gap of unknown length
* 42831
* 43917: contig of 1087 bp in length
* 43918
* 44017: gap of unknown length
* 44018
* 44825: contig of 808 bp in length
* 44826
* 44925: gap of unknown length
* 44926
* 46114: contig of 1189 bp in length
* 46115
* 46214: gap of unknown length
* 46215
* 47031: contig of 817 bp in length
* 47032
* 47131: gap of unknown length
* 47132
* 48292: contig of 1161 bp in length
* 48293
* 48392: gap of unknown length
* 48393
* 49176: contig of 784 bp in length
* 49177
* 49276: gap of unknown length
* 49277
* 50389: contig of 1113 bp in length
* 50390
* 50489: gap of unknown length
* 50490
* 51333: contig of 844 bp in length
* 51334
* 51433: gap of unknown length
* 51434
* 52765: contig of 1332 bp in length
* 52766
* 52865: gap of unknown length
* 52866
* 53810: contig of 845 bp in length
* 53811
* 53910: gap of unknown length
* 53911
* 54965: contig of 1155 bp in length
* 54966
* 55065: gap of unknown length
* 55066
* 55910: contig of 845 bp in length
* 55911
* 56010: gap of unknown length
* 56011
* 57558: contig of 1548 bp in length
* 57559
* 57658: gap of unknown length
* 57659
* 58509: contig of 851 bp in length
* 58510
* 58609: gap of unknown length
* 58610
* 59745: contig of 1136 bp in length
* 59746
* 59845: gap of unknown length
* 59846
* 60655: contig of 810 bp in length
* 60656
* 60755: gap of unknown length
* 60756
* 61976: contig of 1221 bp in length
* 61977
* 62076: gap of unknown length
* 62077
* 62896: contig of 820 bp in length
* 62897
* 62996: gap of unknown length
* 62997
* 64128: contig of 1132 bp in length
* 64129
* 64228: gap of unknown length
* 64229
* 65026: contig of 798 bp in length
* 65027
* 65126: gap of unknown length
* 65127
* 66269: contig of 1143 bp in length
* 66270
* 66369: gap of unknown length
* 66370
* 67220: contig of 851 bp in length
* 67221
* 67320: gap of unknown length
* 67321
* 68425: contig of 1105 bp in length
* 68426
* 68525: gap of unknown length
* 68526
* 69322: contig of 797 bp in length
* 69323
* 69422: gap of unknown length
* 69423
* 70568: contig of 1146 bp in length
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* 70668: gap of unknown length
* 70669
* 71547: contig of 879 bp in length
* 71548
* 71647: gap of unknown length
* 71648
* 73629: contig of 1982 bp in length
* 73630
* 73729: gap of unknown length
* 73730
* 74587: contig of 858 bp in length
* 74588
* 74687: gap of unknown length
* 74688
* 75780: contig of 1093 bp in length
* 75781
* 75880: gap of unknown length
* 75881
* 77196: contig of 1316 bp in length
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\* 77197 77296: gap of unknown length  
\* 77297 78651: contig of 1355 bp in length  
\* 78652 78751: gap of unknown length  
\* 78752 79557: contig of 806 bp in length  
\* 79558 79657: gap of unknown length  
\* 79658 80774: contig of 1117 bp in length  
\* 80775 80875: gap of unknown length  
\* 80875 81690: contig of 816 bp in length  
\* 81691 81790: gap of unknown length  
\* 81791 82928: contig of 1138 bp in length  
\* 82929 83028: gap of unknown length  
\* 83029 83902: contig of 874 bp in length  
\* 83903 84002: gap of unknown length  
\* 84003 85193: contig of 1191 bp in length  
\* 85194 85293: gap of unknown length  
\* 85294 86149: contig of 856 bp in length

Query Match 68.3%; Score 88.8; DB 2; Length 214669;  
Best Local Similarity 85.3%; Pred. No. 3.3e-10;  
Matches 110; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 3 CGCCTACCTGGCTACCCCGGGAACCGCTTGAGCTGTGGGGGCTGATGGGGATTCCGT 62  
LOCUS 93457 CCCTTACCTGGATACCCCGAAACCGCTTGACCTGGTGGCTGATGGGGATTCCGT 93516

QY 63 GCTCTCCGACAGCCCGCGCCCACTT-GGAGNAGTGTGACGCTCGTACCTTCGCAG 121  
Db 93517 ACTCTCCGACAGACCCCGTCCCACTTAGGCAAAAGGAGCGCTCGTACCTTCGAG 93576

QY 122 GACGCTGCT 130  
Db 93577 GACACTTCT 93585

RESULT 9  
AY029163  
LOCUS AY029163 1074 bp mRNA linear ROD 19-JUN-2003  
DEFINITION Rattus norvegicus BCL2L10 (Bcl2l10) mRNA, complete cds.  
ACCESSION AY029163  
VERSION AY029163.1 GI:13641257  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus  
1 (bases 1 to 1074)  
Itoh,T., Itoh,A. and Pleasure,D.  
Bcl-2-related protein family gene expression during  
oligodendroglial differentiation  
J. Neurochem. 85 (6), 1500-1512 (2003)  
JOURNAL 22672518  
MEDLINE 12787069  
PUBMED 2 (bases 1 to 1074)  
Itoh,T., Itoh,A. and Pleasure,D.  
Direct Submission  
TITLE Submitted (29-MAR-2001) Neurology Research, The Children's Hospital  
of Philadelphia, Abramson Research Center, Room 516 I, 3517 Civic  
Center Boulevard, Philadelphia, PA 19104, USA  
FEATURES  
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1. 1074  
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WRRLITAIILISCFPATIPIYIMKCL"

ORIGIN  
Query Match 42.6%; Score 55.4; DB 10; Length 1074;  
Best Local Similarity 69.8%; Pred. No. 0.018;  
Matches 88; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 3 CGCCTACCTGGCTACCCCGGGAACCGCTTGAGCTGTGGGGGCTGATGGGGATTCCGT 62  
Db 176 CTCCTCCGACAGACCCCGGCAACCGCTGAGCTGTGACAGATGGCGGATGATT 235

QY 63 GCTCTCCGACAGCCCGCGCCCACTT-GGAGNAGTGTGACGCTCGTACCTTCGCAG 121  
Db 236 GCTCTCAATGACCAAGATTCACTGGAGCCCGCTGTGATGCTCTTGAGCTTCGTGGG 295

QY 122 GACGCT 127  
Db 296 GACGCT 301

RESULT 10  
AC11669 240461 bp DNA linear HTG 09-NOV-2002  
LOCUS AC11669  
DEFINITION Rattus norvegicus clone CH230-54110, WORKING DRAFT SEQUENCE, 5  
unordered pieces.  
ACCESSION AC11669.4 GI:24818904  
VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus  
1 (bases 1 to 240461)  
Muzny,D.,Marie.,Mezker,M.,Lee.,Abramson,S.,Adams,C.,Alder,J.,  
Allen,C.,Allen,H.,Alabrooks,S.,Amn,A.,Angiano,D.,  
Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Bacc,E.,Baden,H.,  
Baldwin,D.,Bandaranatke,D.,Barber,M.,Barnstead,M.,Benahmed,F.,  
Blewett,K.,Blair,J.,Blankenbury,K.,Blyth,P.,Brown,M.,  
Bryant,N.,Buhay,C.,Burck,P.,Buttill,K.,Calderson,E.,  
Cardenas,V.,Carter,K.,Cavazos,I.,Cesari,H.,Center,A.,  
Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,  
Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,  
Devila,M.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,  
Deigado,O.,Denson,S.,Deramo,C.,Ding,Y.,Dinh,H.,Divya,K.,  
Draper,H.,Dugan-Rocha,S.,Dunn,A.,Dublin,K.,Duval,B.,Eaves,K.,  
Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G.,  
Fernandez,S.,Finley,M.,Flagg,N.,Forbes,L.,Foster,M.,Foster,P.,  
Fraser,C.M.,Gabisi,A.,Ganta,R.,Garcia,A.,Garner,T.,Garrar,M.,  
Georgievski,E.,Geier,K.,Gill,R.,Grady,M.,Guerra,W.,Guevara,M.,  
Gunaratne,P.,Haaland,W.,Hamill,C.,Hamilton,C.,Hamilton,K.,  
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Hollins,B.,Howells,J.,Huliyk,S.,Hume,J.,Idlebird,D.,Jackson,A.,  
Jackson,L.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolivet,A.,  
Karpachy,S.,Kelly,S.,Kelly,S.,Khan,Z.,King,L.,Koyat,C.,  
Kowis,C.,Kraft,C.L.,Lebow,H.,Levan,J.,Lewis,L.,Li,Z.,Liu,J.,  
Liu,J.,Liu,W.,Liu,Y.,London,P.,Longacre,S.,Lopez,J.,  
Lorenshewa,L.,Louissegel,H.,Lopez,R.J.,Lu,X.,Ma,J.,  
Maheshwari,M.,Mahindartine,M.,Mahmoud,M.,Malloy,K.,Mangum,A.,  
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Mawhiney,S.,McLeod,M.P.,McNeill,T.Z.,Meenen,E.,  
Milosavljevic,A.,Miner,G.,Minja,E.,Montemayor,J.,Moore,S.,  
Morgan,M.,Morris,K.,Morris,S.,Munidesa,M.,Murphy,M.,Nair,L.,  
Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,  
Nwokilemeh,O.,Okunnu,G.,Olanunnsagun,A.,Pal,S.,Parke,K.,  
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Plopper,F.,Polidexter,A.,Popovic,D.,Pyrimus,B.,Pu,L.,L.,  
Puzo,M.,Quitroz,J.,Rachlin,E.,Reeves,K.,Regier,M.A.,Reigh,R.,

Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,  
Rivas, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,  
Sander, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,  
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smajda, D.,  
Sned, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,  
Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,  
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemami, K.,  
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,  
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,  
Williams, G., Willson, R., Wlezyk, R., Woodem, H., Worley, K.,  
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,  
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von  
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
Weinstock, G. and Gibbs, R. A.

Direct Submission  
Unpublished  
2 (bases 1 to 240461)  
Worley, K. C.

Direct Submission  
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 240461)  
Rat Genome Sequencing Consortium.

Submitted (09-NOV-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2002 this sequence version replaced gi:23196052.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GNVB  
Center clone name: CH230-54110  
----- Summary Statistics  
Assembly program: Phrap, version 0.990329  
Consensus quality: 218898 bases at least Q40  
Consensus quality: 223128 bases at least Q20  
Consensus quality: 223928 bases at least Q20  
Estimated insert size: 223140; sum-of-contigs estimation  
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_diff\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 9792: contig of 9792 bp in length  
\* 9793 9892: gap of unknown length  
\* 9893 118024: contig of 108133 bp in length  
\* 118025 118124: gap of unknown length  
\* 118125 236958: contig of 118833 bp in length  
\* 236959 237058: gap of unknown length

237059 238398: contig of 1340 bp in length  
\* 238399 238498: gap of unknown length  
\* 238499 240461: contig of 1963 bp in length.

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\* 238499 240461: contig of 1963 bp in length.  
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/clone="CH230-54110"  
1. 1351  
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6797. 7581  
/note="clone boundary  
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site:ECORI  
end\_sequence:BH349014"  
8640. 9792  
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118125. 119133  
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misc\_feature  
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misc\_feature

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Best Local Similarity 69.8%; Pred. No. 0.0073;  
Matches 88; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 3 CGCTCACTCGGCTACCCCGGAAACCGTTGAGCTGTGGCGCTGATGCGGATTCCT 62  
DB 21975 CTCCTTCGCGACATACCGGCGCAACCGCTGTGACATGTCACAGATGGCGATGAGTT 22034  
QY 63 GCTCTCGGACGACCCCGGCCCACTT-GGGAGNAGTGTGAGCGCTCGTACCTTCGACG 121  
DB 22035 GCTTCATATACCAAGATTCACTGGGCGCCGCTGTGATCTCTGCGCTTGTCG 22094  
QY 122 GACGCT 127  
DB 22095 GACGCT 22100

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RESULT 11  
AF102501 1209 bp mRNA linear ROD 21-JAN-1999  
LOCUS AF102501 Mus musculus Bcl-2 homolog (bcl-2) mRNA, complete cds.  
DEFINITION AF102501  
ACCESSION AF102501.1 GI:4165137  
VERSION AF102501.1  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

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REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE Song, Q.-Z., Kuang, Y. P., Dixit, V. M. and Vincenz, C.  
1 (bases 1 to 1209)  
BOO, a novel negative regulator of cell death, interacts with  
Apaf-1  
EMBO J 18 (1), 167-178 (1999)  
MEDLINE 99094902  
PUBMED 9878060

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REFERENCE  
AUTHORS 2 (bases 1 to 1209)  
TITLE Song, Q.-Z., Kuang, Y. P., Dixit, V. M. and Vincenz, C.  
Direct Submission  
JOURNAL Submitted (28-OCT-1998) Pathology, University of Michigan, 1301  
Catherine Road, Ann Arbor, MI 48109, USA  
FEATURES  
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1. 1209  
gene

	/gene="Boo"
CDS	117. .692

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Best Local Similarity	67.2%	Pred. No. 0.16;		
Matches	86;	Conservative	0;	Mismatches 41;
			Indels	1;
			Gaps	1;

Db 408 GGGACGCT 415

RESULT 12	LOCUS	DEFINITION	ACCSSION	VERSION
AF067660	AF067660	Mus musculus Bcl-2 homolog (D1va)	1225 bp mRNA	linear ROD 04-DEC-1999
			AF067660.1	GI:3955265

FEATURES	Location/Qualifiers
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polya_signal	polya_site
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## ORIGIN

Query Match	39.2%	Score 51;	DB 10;	Length 1225;
Best Local Similarity	67.2%	Pred. No. 0.16;		
Matches	86;	Conservative	0;	Mismatches 41;
				Indels 1;
				Gaps 1;

Db 434 GGGACGCT 441

RESULT	13
BC052690	
LOCUS	1257 bp mRNA linear ROD 08-OCT-2003
DEFINITION	Mus musculus Bcl2-like 10, mRNA (CDNA clone MGC:60542 IMAGE:30052580), complete cds.
ACCESSION	BC052690
VERSION	BC052690.1 GI:30851238
KEYWORDS	MGC.
SOURCE	Mus musculus (house mouse)

REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: nisc\_mgc@nsl.nih.gov

Alkner, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooke, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
Hansen, N., Ho, S.-L., Karlin, S., Kwong, P., Latic, P., Legaspi, R.,  
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W.,  
Taurgeson, C., Vogt, J.L., Walker, M.A., Weherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>  
Series: IRAC Plate: 112 Row: h Column: 18  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 7304926.

## FEATURES

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(Long)"  
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/note="Vector: pSPORT1"

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/db\_xref="MGI:1330841"  
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## CDS

## misc\_feature

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/db\_xref="CCDD:smart00337"

## ORIGIN

Query Match 39.2%; Score 51; DB 10; Length 1257;  
Best Local Similarity 67.2%; Pred. No. 0.16;  
Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

1 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCAGCTGTGGCGCTGATGCGGATTC 60  
|||  
Db 316 TCCCTCTTCGCAAGACCGGGGCAATGCTGAGCTGGTGAAGACATGACATTAAG 375  
|||  
Qy 61 GTGCTTCGCAAGACCGGGGCAATGCTGAGCTGGTGAAGACATGACATTCGCA 119  
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Db 376 TTGCTCTCAAGACCAAGACTTCACTGAGCGAGCAACTGTGATGCTCTGCGCG 435  
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Qy 120 GGAAGCGT 127  
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Db 436 GGAAGCGT 443  
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## RESULT 14

AC133947  
LOCUS AC133947 168997 bp DNA linear ROD 08-SEP-2004  
DEFINITION Mus musculus chromosome 9 clone RP24-16912, complete sequence.  
ACCESSION AC133947  
VERSION AC133947.3 GI:51921460  
KEYWORDS HTG.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Wilson, R.K.  
TITLE The sequence of Mus musculus clone  
JOURNAL Unpublished  
2 (bases 1 to 168997)  
AUTHORS McPherson, J.D. and Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
3 (bases 1 to 168997)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUL-2004) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
4 (bases 1 to 168997)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-2004) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
On Sep 8, 2004 this sequence version replaced gi:50199129.

## COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu>  
Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
Project Information  
Center project name: M\_BB0189102  
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## FEATURES

Location/Qualifiers  
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/clone="RP24-16912"

## source

Query Match 39.2%; Score 51; DB 10; Length 168997;  
Best Local Similarity 67.2%; Pred. No. 0.072;  
Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

## ORIGIN

1 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCAGCTGTGGCGCTGATGCGGATTC 60  
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Db 166643 TTGCTCTCAAGACCAAGACTTCACTGAGCGAGCAACTGTGATGCTCTGCGCG 166702  
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Qy 120 GGAAGCGT 127  
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Db 166703 GGAAGCGT 166710  
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## RESULT 15

AC115880 202851 bp DNA linear ROD 02-APR-2004  
DEFINITION Mus musculus chromosome 9, clone RP24-365N15, complete sequence.  
ACCESSION AC115880  
VERSION AC115880.11 GI:46063808  
KEYWORDS HTG.  
SOURCE Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 202851)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCES  
AUTHORS  
Mus musculus chromosome 9, clone RP24-365N1S  
Unpublished  
2 (bases 1 to 202851)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunthang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G., Zainoun, O., Zemdek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 202851)  
REFERENCE  
AUTHORS  
Birren, B., Nusbaum, C., Lander, E., Abouelkell, A., Allen, N., Anderson, M., Archchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunthang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (28-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
4 (bases 1 to 202851)  
REFERENCE  
AUTHORS  
Birren, B., Nusbaum, C., Lander, E., Abouelkell, A., Allen, N., Anderson, M., Anderson, S., Archchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunthang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,

Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (02-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 2, 2004 this sequence version replaced gi:44681569.  
All repeats were identified using RepeatMasker:  
Smit, A.P. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
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Genome Center  
Center: Whitehead Institute/MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@broad.mit.edu  
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Project Information  
Center project name: L24773  
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Query Match 39.2%; Score 51; DB 10; Length 202851;

Best Local Similarity 67.2%; Pred. No. 0.069; Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

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QY      1  TCCGCTACTCGGCTACCCGCGAACCCTTCGAGCTGTGTGCGCTGATGGCGGATTCC 60
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QY      120 GGGACGCT 127
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Job time : 1004.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2005, 08:53:44 ; Search time 127.188 Seconds  
(without alignment)

6050.630 Million cell updates/sec

Title: US-10-071-174A-37

Perfect score: 130

Sequence: 1 tcgcgcaccccgctacc.....acctcgacggagcgtgct 130

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N Geneseq 16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114.8	88.3	582	3	AAZ90039 Hydrophob
2	114.8	88.3	887	6	AAD46683 Human Bcl
3	114.8	88.3	1168	3	AAZ90049 Hydrophob
4	100.8	77.5	548	4	ABK41913 CDNA enco
5	100.8	77.5	548	9	ADB59580 Connectiv
6	86.8	66.8	522	4	AAH47022 Human Bcl
7	73.2	56.3	874	6	ABQ44403 Oligonuc
8	73.2	56.3	874	6	ABQ44402 Oligonuc
9	62	47.7	874	6	ABQ44404 Oligonuc
10	62	47.7	874	6	ABQ44405 Oligonuc
11	51	39.2	650	10	ADD34132 Mouse mlt
12	36.8	28.3	3288	2	AAZ33800 Murine in
13	36.8	28.3	3288	2	AAV27591 Mouse int
14	36.8	28.3	3288	2	AAV01921 Murine IL
15	36.8	28.3	3288	3	AAAS1987 Murine in
16	36.8	28.3	3288	3	AAAS2145 Murine in
17	36.8	28.3	3288	3	AAAS9870 Murine in
18	36.8	28.3	3288	3	AAAG1238 Murine IL
19	36.8	28.3	3288	4	AAAF57186 Murine IL
20	36.8	28.3	3288	4	AAD02813 Murine in

C	21	36.8	28.3	3288	12	ADJ88256	Adj88256 Murine IL
C	22	36.8	28.3	3288	12	ADQ91243	Adq91243 Mouse CDN
C	23	36.8	28.3	3288	12	ADR01299	Adr01299 Mouse int
C	24	35.4	27.2	1724	6	ABA01821	AbA01821 Rice Brar
C	25	35.4	27.2	2412	10	ADC07863	AdC07863 Rice DNA
C	26	35.4	27.2	2412	12	ADJ40034	AdJ40034 Plant CDN
C	27	35.4	27.2	2607	8	ACC70868	Acc70868 Rice Brar
C	28	35.4	27.2	2607	8	ACC70869	Acc70869 Rice Brar
C	29	35.4	27.2	5928	8	ACC70867	Acc70867 Rice Brar
C	30	35.4	27.2	5935	8	ACC70866	Acc70866 Rice Brar
C	31	34.8	26.8	1455	8	ADA70199	Ada70199 Rice gene
C	32	33.8	26.0	24379	2	AAV93095	AAV93095 Streptomy
C	33	33.8	26.0	24379	2	AAV25925	AAV25925 Streptomy
C	34	33.6	25.8	1077	9	ADA48367	Ada48367 Rice gene
C	35	33.6	25.8	1077	12	ADJ39313	AdJ39313 Plant CDN
C	36	33.4	25.7	1125	2	AAQ36369	AAQ36369 T.thermop
C	37	33.4	25.7	1759	10	ABZ57164	ABZ57164 Human met
C	38	33	25.4	1911	6	ABZ78669	ABZ78669 S. ghanae
C	39	32.6	25.1	47988	10	ADB66070	ADB66070 Streptomy
C	40	32.4	24.9	675	12	ADQ75857	AdQ75857 Barley ly
C	41	32.2	24.8	792	4	AAH70552	AAH70552 Human cer
C	42	32.2	24.8	17083	10	ABZ58812	ABZ58812 S. cinna
C	43	32	24.6	992	4	ABL12245	ABl12245 Drosophi
C	44	32	24.6	2859	10	ADF30786	Adf30786 Soil meta
C	45	32	24.6	3486	8	ABQ77425	AbQ77425 Human GCD

## ALIGNMENTS

RESULT 1	AAZ90039	standard; CDNA, 582 BP.
XX	AAZ90039;	
XX	09-MAY-2000	(first entry)
DE	Hydrophobic domain containing protein clone HP02403 coding sequence.	
XX	Hydrophobic domain; clone HP02403; nutritional supplement; SCID; HIV;	
XX	cell proliferation; immune stimulant; immune deficiency; tumour; pain;	
XX	rheumatoid arthritis; insulin dependent diabetes mellitus; fertility;	
KW	myaethenia gravis; haematopoiesis regulator; tissue growth; depression;	
KM	anti-inflammatory; infection; bodily characteristic; ss.	
OS	Homo sapiens.	
XX	MO20000506-A2.	
PD	06-JAN-2000.	
XX	18-JUN-1999;	99WO-JP003242.
PF	26-JUN-1998;	98JP-00180008.
PR	(SAGA ) SAGAMI CHEM RES CENT.	
PA	(PROT-) PROTEGENE INC.	
XX	Kato S, Kimura T;	
PI	WPI, 2000-160665/14.	
DR	P-PSDB; AAV78802.	
DR	Novel human proteins having hydrophobic domains used for research and	
PT	diagnostic purposes.	
PS	Claim 3; Page 84; 117pp; English.	
XX	This sequence represents the hydrophobic domain containing protein, clone	
CC	HP00631 coding region. The sequence is isolated from a human stomach	
CC	cancer cell line. The HP02403 protein contains one putative transmembrane	
CC	domain. The protein shows homology to the Japanese quail apoptosis	

CC regulator NR-13. The invention relates to human proteins with hydrophobic domains, the DNA and the cDNA encoding them. The polynucleotides and proteins are predicted to have biological activities which make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity (nutritional source or supplement); cytokine and cell proliferation/differentiation activity; immune stimulating (e.g. as vaccines) or suppressing activity (e.g. to treat various immune deficiencies such as SCIDS or HIV, connective tissue disease, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease, as well as asthma, allergies and organ transplantation); haematopoiesis regulating activity (e.g. in treatment of myeloid or lymphoid cell deficiencies); tissue growth activity (e.g. wound healing and tissue repair, ulcers, burns, periodontal disease); activin/inhibin activity; chemocactive/chemokinetic activity; haemostatic and thrombolytic activity (e.g. treating haemophilias); receptor/ligand activity; anti-inflammatory activity; and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. Other activities include inhibiting infections caused by bacteria, fungi, viruses and other parasites (e.g. Hepatitis, malaria); affecting bodily characteristics such as, e.g. weight, colour, skin, affecting biorhythms or circadian cycles; enhancing fertility; treatment of depression; treatment of pain; hormonal or endocrine activity. The polynucleotides may also be used for recombinant expression of the protein

CC XX Sequence 582 BP; 85 A; 193 C; 191 G; 113 T; 0 U; 0 Other;

Query Match 88.3%; Score 114.8; DB 3; Length 582;

Best Local Similarity 96.9%; Pred. No. 1.6e-19;

Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 163 TCCGCTACTCTGGGTACCCCGGGAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 222

QY 61 GTGCTCTCCGACAGCCCGGAGCCGACCT-GGGAGNAGTGTGACGCTGTGACCTTCGCA 119  
DB 223 GTGCTCTCCGACAGCCCGGAGCCGACCTGTGAGGACAGTGTGACGCTGTGACCTTCGCA 282

QY 120 GGGACGCTGCT 130  
DB 283 GGGACGCTGCT 293

RESULT 2  
AAD46683 standard; DNA; 887 BP.

XX AAD46683;

DT 27-JAN-2003 (first entry)

DE Human Bcl-B DNA.

XX Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder; proliferative disorder; muscle degeneration; Alzheimer's disease; CJD; Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic; Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia; SCA; dentatorubropallidoluylian atrophy; DRPLA; Kennedy's disease; stroke; ischaemia; head trauma; neoplasia; anticonvulsant; vulnerary; neurotropic; neuroprotective; cytosstatic; immunosuppressive; vasotropic; cerebroprotective; autoimmune disorder; chromosome 15; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 50..664

FT /\*tag= a

XX /product= "Human Bcl-B protein"

PN W0200272601-A2.

XX 19-SEP-2002.

XX 07-FEB-2002; 2002WO-US003547.

XX 07-FEB-2001; 2001US-0267166P.

PR 07-FEB-2002; 2002US-00071174.

XX (BURN-) BURNHAM INST.

PI Reed JC, Ke N, Godzik A;

DR WPI; 2002-723312/78.

PT P-PSDB; AAE29097.

PT New isolated or recombinant Bcl-B nucleic acids and polypeptides, for treating a disorder associated with apoptosis, such as cell degenerative or proliferative disorder e.g. cancer, Alzheimer's disease or Parkinson's disease.

XX PS Claim 11; Page 74; 82pp; English.

XX The invention relates to human member of Bcl-2 family Bcl-B protein and its corresponding nucleic acid. Bcl-B is useful in treating a subject having or at risk of a disorder associated with apoptosis, such as cell degenerative or proliferative disorder like neural or muscle degeneration, e.g. Alzheimer's disease, Creutzfeldt-Jacob's disease (CJD), Machado-Joseph disease (MJD), Parkinson's disease, Huntington's disease (HD), spinocerebellar ataxias 1, 2 and 6 (SCA-1, -2 and -6), dentatorubropallidoluylian atrophy (DRPLA), Kennedy's disease, stroke, ischaemia, head trauma, neoplasia, autoimmune disorder or fibrotic condition. The transgenic animals are used as in vivo models to study apoptosis and potential therapies for apoptosis. The present sequence is human Bcl-B DNA. Bcl-B gene is located at chromosome 15

XX SQ Sequence 887 BP; 171 A; 270 C; 269 G; 177 T; 0 U; 0 Other;

Query Match 88.3%; Score 114.8; DB 6; Length 887;

Best Local Similarity 96.9%; Pred. No. 1.6e-19;

Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 TCCGCTACTCTGGGTACCCCGGGAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 60  
DB 242 TCCGCTACTCTGGGTACCCCGGGAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 301

QY 61 GTGCTCTCCGACAGCCCGGAGCCGACCT-GGGAGNAGTGTGACGCTGTGACCTTCGCA 119  
DB 302 GTGCTCTCCGACAGCCCGGAGCCGACCTGTGAGGACAGTGTGACGCTGTGACCTTCGCA 361

QY 120 GGGACGCTGCT 130  
DB 362 GGGACGCTGCT 372

RESULT 3  
AAZ90049 standard; cDNA; 1168 BP.

XX AAZ90049;

DT 09-MAY-2000 (first entry)

DE Hydrophobic domain containing protein clone HP02403 nucleotide sequence.

XX Hydrophobic domain; clone HP02403; nutritional supplement; SCID; HIV;

XX cell proliferation; immune stimulant; immune deficiency; tumour; pain;

XX rheumatoid arthritis; insulin dependent diabetes mellitus; fertility;

XX myasthenia gravis; haematopoiesis regulator; tissue growth; depression;

XX anti-inflammatory; infection; bodily characteristic; ss.

XX Homo sapiens;

PN WO20000506-A2.  
XX 06-JAN-2000.  
PD 18-JUN-1999; 99WO-JP003242.  
XX 26-JUN-1998; 98JP-00180008.  
XX (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
XX Kato S, Kimura T;  
XX WPI; 2000-160665/14.  
DR P-PSDB; AAV78802.  
PT Novel human proteins having hydrophobic domains used for research and  
XX diagnostic purposes.  
PS Claim 4; Page 92-94; 117pp; English.  
XX This sequence represents the hydrophobic domain containing protein, clone  
CC HP00631 nucleotide sequence. The sequence is isolated from a human  
CC stomach cancer cell line. The HP02403 protein contains one putative  
CC transmembrane domain. The protein shows homology to the Japanese quail  
CC apoptosis regulator NR-13. The invention relates to human proteins with  
CC hydrophobic domains, the DNA and the cDNA encoding them. The  
CC polynucleotides and proteins are predicted to have biological activities  
CC which make them suitable for treating, preventing or ameliorating medical  
CC conditions in humans and animals. Suggested activities include  
CC nutritional activity (nutritional source or supplement); cytokine and  
CC cell proliferation/differentiation activity; immune stimulating (e.g. as  
CC vaccines) or suppressing activity (e.g. to treat various immune  
CC deficiencies such as SCIDS or HIV, connective tissue disease, systemic  
CC lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary  
CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin  
CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease  
CC and autoimmune inflammatory eye disease, as well as asthma, allergies and  
CC organ transplantation); haematopoiesis regulating activity (e.g. in  
CC treatment of myeloid or lymphoid cell deficiencies); tissue growth  
CC activity (e.g. wound healing and tissue repair, ulcers, burns,  
CC periodontal disease); activin/inhibin activity; chemotactic/chemokinetic  
CC activity; haemostatic and thrombolytic activity (e.g. treating  
CC haemophilias); receptor/ligand activity; anti-inflammatory activity; and  
CC tumour inhibition activity. The polynucleotides are also stated to be  
CC useful for gene therapy. Other activities include inhibiting infections  
CC caused by bacteria, fungi, viruses and other parasites (e.g. Hepatitis,  
CC malaria); effecting bodily characteristics such as, e.g. weight, colour,  
CC skin, effecting biohythms or circadian cycles; enhancing fertility;  
CC treatment of depression; treatment of pain; hormonal or endocrine  
CC activity. The polynucleotides may also be used for recombinant expression  
CC of the protein.  
XX  
SQ Sequence 1168 BP; 276 A; 312 C; 300 G; 280 T; 0 U; 0 Other;  
Query Match 88.3%; Score 114.8; DB 3; Length 1168;  
Best Local Similarity 96.9%; Pred. No. 1.6e-19;  
Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 TCCGCTCACTCGGTACCCGGGAAACGCTTCGAGCTGTGGCGCTGATTC 60  
Db 169 TCCGCTCACTCGGTACCCGGGAAACGCTTCGAGCTGTGGCGCTGATTC 228  
QY 61 GTGCTCTCGACAGCCCGGCGCCACCT-GGGAGNAGTGTGACGCTGTCGCA 119  
Db 229 GTGCTCTCGACAGCCCGGCGCCACCTGTGGGCAAGTGTGACGCTGTCGCA 288  
QY 120 GGGACGCTGCT 130  
Db 289 GGGACGCTGCT 299

RESULT 4

ABK41913  
ID ABK41913 standard; cDNA, 548 BP.  
XX AC ABK41913;  
XX DT 21-MAY-2002 (first entry)  
DE cDNA encoding novel human connective tissue related polypeptide #301.  
XX Human; connective tissue related disorder; cancer; gene therapy;  
XX cytoskeletal; gene; ss.  
OS Homo sapiens.  
XX WO200155343-A1.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US001322.  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 24-FEB-2000; 2000US-0184664P.  
XX 02-MAR-2000; 2000US-0186350P.  
XX 16-MAR-2000; 2000US-0189874P.  
XX 17-MAR-2000; 2000US-0190076P.  
XX 18-APR-2000; 2000US-0198123P.  
XX 19-MAY-2000; 2000US-0205515P.  
XX 07-JUN-2000; 2000US-0209467P.  
XX 28-JUN-2000; 2000US-0214886P.  
XX 30-JUN-2000; 2000US-0215135P.  
XX 07-JUL-2000; 2000US-0216647P.  
XX 07-JUL-2000; 2000US-0216880P.  
XX 11-JUL-2000; 2000US-0217487P.  
XX 11-JUL-2000; 2000US-0217496P.  
XX 16-JUL-2000; 2000US-0218290P.  
XX 26-JUL-2000; 2000US-0220963P.  
XX 26-JUL-2000; 2000US-0220964P.  
XX 14-AUG-2000; 2000US-0224518P.  
XX 14-AUG-2000; 2000US-0224519P.  
XX 14-AUG-2000; 2000US-0225213P.  
XX 14-AUG-2000; 2000US-0225214P.  
XX 14-AUG-2000; 2000US-0225266P.  
XX 14-AUG-2000; 2000US-0225267P.  
XX 14-AUG-2000; 2000US-0225268P.  
XX 14-AUG-2000; 2000US-0225270P.  
XX 14-AUG-2000; 2000US-0225447P.  
XX 14-AUG-2000; 2000US-0225757P.  
XX 14-AUG-2000; 2000US-0225758P.  
XX 14-AUG-2000; 2000US-0225759P.  
XX 18-AUG-2000; 2000US-0226279P.  
XX 22-AUG-2000; 2000US-0226681P.  
XX 22-AUG-2000; 2000US-0226868P.  
XX 23-AUG-2000; 2000US-0227182P.  
XX 23-AUG-2000; 2000US-0227009P.  
XX 30-AUG-2000; 2000US-0228924P.  
XX 01-SEP-2000; 2000US-0229287P.  
XX 01-SEP-2000; 2000US-0229343P.  
XX 01-SEP-2000; 2000US-0229344P.  
XX 01-SEP-2000; 2000US-0229345P.  
XX 05-SEP-2000; 2000US-0229509P.  
XX 05-SEP-2000; 2000US-0229513P.  
XX 06-SEP-2000; 2000US-0230437P.  
XX 06-SEP-2000; 2000US-0230438P.  
XX 08-SEP-2000; 2000US-0231242P.  
XX 08-SEP-2000; 2000US-0231243P.  
XX 08-SEP-2000; 2000US-0231244P.  
XX 08-SEP-2000; 2000US-0231413P.  
XX 08-SEP-2000; 2000US-0231414P.  
XX 08-SEP-2000; 2000US-0232081P.  
XX 12-SEP-2000; 2000US-0231968P.  
XX 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0233398P.  
 PR 14-SEP-2000; 2000US-0233399P.  
 PR 14-SEP-2000; 2000US-0233400P.  
 PR 14-SEP-2000; 2000US-0233401P.  
 PR 14-SEP-2000; 2000US-0233402P.  
 PR 14-SEP-2000; 2000US-0233403P.  
 PR 14-SEP-2000; 2000US-0233404P.  
 PR 14-SEP-2000; 2000US-0233405P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234224P.  
 PR 21-SEP-2000; 2000US-0234225P.  
 PR 25-SEP-2000; 2000US-0234977P.  
 PR 25-SEP-2000; 2000US-0234978P.  
 PR 26-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 27-SEP-2000; 2000US-0235835P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 13-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239335P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 20-OCT-2000; 2000US-0241826P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249246P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.

PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Barash SC, Ruben SM;  
 XX  
 XX WPI; 2001-565190/63.  
 DR P-PSDB; AAU86735.  
 DR  
 XX  
 PT Nucleic acid encoding novel connective tissue associated polypeptides,  
 PT used in diagnosing, preventing, treating or ameliorating a disorder such  
 PT as cancer or rheumatoid arthritis.  
 XX  
 PS Claim 4; SEQ ID NO 311; 673bp; English.  
 XX  
 CC The present invention relates to the isolation of novel human connective  
 CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide  
 CC (cDNA and genomic) sequences encoding them. The sequences of the  
 CC invention are useful in the diagnosis, treatment, prevention and/or  
 CC prognosis of diseases associated with connective tissue(s), including  
 CC cancer. The polynucleotide sequences of the invention are also useful in  
 CC gene therapy. ABK41613-ABK42101 represent cDNA sequences encoding the  
 CC novel human connective tissue related polypeptides. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_ptc\_sequences  
 CC  
 XX  
 SQ Sequence 548 BP; 99 A; 154 C; 167 G; 121 T; 0 U; 7 Other;  
 Query Match 77.5%; Score 100.8; DB 4; Length 548;  
 Best Local Similarity 92.9%; Pred. No. 5e-16; 8; Indels 0; Gaps 0;  
 Matches 105; Conservative 0; Mismatches 8  
 QY 18 CCGCGGAAACCGCTTCGAGTGTGGCGCTGATGCGCGATTCCGTCTCCGACAGCCC 77  
 Db 61 CCACGCGTCGCGCTTCGAGTGTGGCGCTGATGCGCGATTCCGTCTCCGACAGCCC 120  
 QY 78 CCGCGGCACTGCGAGAGAGTGTGACGCTCGTGAACCTTCGAGGAGCGCTGCT 130  
 Db 121 CCGCGGCACTGCGAGAGTGTGACGCTCGTGAACCTTCGAGGAGCGCTGCT 173  
 RESULT 5  
 ADB59580  
 ID ADB59580 standard; cDNA; 548 BP.  
 XX  
 AC ADB59580;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Connective tissue related polynucleotide #301.  
 XX  
 KW cytosolic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;  
 KW antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritis;  
 KW antiinflammatory; antiallergic; antilastmatic; dermatological;  
 KW nephrotoxic; virucide; fungicide; antibacterial; antiparasitic;  
 KW gene therapy; ds; connective tissues disorder; rheumatoid arthritis;  
 KW systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;  
 KW cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;  
 KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;  
 KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;  
 KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;  
 KW gastrointestinal disorder; inflammatory bowel disease;



PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
PR 17-JAN-2001; 2001US-00764847.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM, Barash SC;  
XX  
DR WPI: 2003-634869/60.  
DR P-PSDB; ADB60069.  
XX  
PT New connective tissue-related polypeptides and polynucleotides, useful  
PT for treating, preventing and/or prognosing e.g. disorders of connective  
PT tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or  
PT neoplasias.  
XX  
PS Claim 1; SEQ ID NO 311; 248bp; English.  
XX  
CC The invention describes an isolated nucleic acid molecule (1), which  
CC comprises a sequence that is at least 95 % identical to a connective  
CC tissue-related polynucleotide encoding connective tissue antigens (CTA).  
CC The polypeptide or polynucleotide is useful for preventing, treating, or  
CC ameliorating medical conditions in a mammal. The connective tissue  
CC polypeptides, polynucleotides and antibodies are particularly useful for  
CC treating, preventing and/or prognosing disorders of connective tissues  
CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,  
CC scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or  
CC neoplasias (e.g. leukemia), neurodegenerative disorders (e.g.  
CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases  
CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass  
CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,  
CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.  
Query Match 77.5%; Score 100.8; DB 9; Length 548;  
Best Local Similarity 92.9%; Pred. No. 5e-16;  
Matches 105; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 18 CCCCCGGAACGCTTCGAGCTGTGGCGCTGATGCGGATTCCTCCGACAGCC 77  
DB 61 CCAACCGCTGGCTTCGAGCTGTGGCGCTGATGCGGATTCCTCCGACAGCC 120  
QY 78 CGGCCCCAAGCTGTGAGCGCTTCGACCTTCGACGAGGACCTGCT 130  
DB 121 CGGCCCCAAGCTGTGAGCGCTTCGACCTTCGACGAGGACCTGCT 173  
RESULT 6  
AAH47022  
ID AAH47022 standard; cDNA; 522 BP.  
XX  
AC AAH47022;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Human Bcl-2-like polypeptide encoding cDNA (clone HLIBE40).  
XX  
KW Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;  
KW respiratory; cardiovascular; antiarthritic; immunostimulant; vaccine;  
KW immunosuppressive; antiinflammatory; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 44..448  
FT /\*tag= a  
FT /product= "Bcl-2-like polypeptide"  
FT /note= "gene No. 2"  
XX  
PN WO200157060-A1.  
XX  
PD 09-AUG-2001.

XX  
PF 31-JAN-2001; 2001WO-US003080.  
XX  
XX  
PR 01-FEB-2000; 2000US-0179487P.  
PR 07-FEB-2000; 2000US-0180697P.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Duan DR, Ni J;  
XX  
DR WPI: 2001-476279/51.  
DR P-PSDB; AAB85666.  
XX  
PT Nucleic acids encoding human Bcl-2-like polypeptides, useful for  
PT preventing, diagnosing and/or treating.  
XX  
PS Claim 1; Page 276; 285pp; English.  
XX  
CC The invention provides nucleic acid molecules (NAM1) encoding a human Bcl  
CC -2-like polypeptides (PEP1). The NAM1 and PEP1 may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate Bcl-2-like polypeptides' expression. The NAM1 may be used  
CC to produce the soluble Bcl-2-like polypeptides by standard recombinant  
CC methodology. The polypeptides may also be used as antigens in the  
CC production of antibodies against Bcl-2 and in assays to identify  
CC modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies  
CC and antagonists may be used to down regulate expression and activity. The  
CC anti-PEP1 antibodies may also be used as diagnostic agents for detecting  
CC the presence of Bcl-2 polyps in samples (e.g. by enzyme linked  
CC immunosorbent assay (ELISA)). Disorders that may be prevented, diagnosed  
CC and/or treated by the above methods include, immunodeficiencies (e.g. a  
CC gammaglobulinemia and B cell lymphoproliferative disorder), autoimmune  
CC disorders (e.g. rheumatoid arthritis and Grave's disease), allergic  
CC reactions, inflammations, respiratory diseases and cardiovascular  
CC disorders (a full list of disorders is given in the specification). The  
CC present sequence represents a human Bcl-2-like polypeptide encoding cDNA  
SQ Sequence 522 BP; 102 A; 148 C; 154 G; 118 T; 0 U; 0 Other;  
Query Match 66.8%; Score 86.8; DB 4; Length 522;  
Best Local Similarity 96.1%; Pred. No. 1.6e-12;  
Matches 99; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 29 GCTTCGAGCTGTGGCGCTGATGCGGATTCCTCCGACAGCCCGGACCACT 88  
DB 1 GCTTCGAGCTGTGGCGCTGATGCGGATTCCTCCGACAGCCCGGACCACT 60  
QY 89 -GGAGNAGTGTGACGCTTCGACCTTCGACGAGGACCTGCT 130  
DB 61 GGGGCAAGTGTGACGCTTCGACCTTCGACGAGGACCTGCT 103  
RESULT 7  
ABQ44403  
ID ABQ44403 standard; DNA; 874 BP.  
XX  
AC ABQ44403;  
XX  
DT 12-JUL-2002 (first entry)  
XX  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 30994.  
XX  
KW Human: cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 44..448  
FT /\*tag= a  
FT /product= "Bcl-2-like polypeptide"  
FT /note= "gene No. 2"  
XX  
PN WO200218632-A2.  
XX  
PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP010074.  
XX  
XX 01-SEP-2000; 2000DE-01043826.  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX WPI; 2002-371829/40.  
DR  
XX  
XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
XX Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
XX Sequence 874 BP; 374 A; 291 C; 90 G; 119 T; 0 U; 0 Other;  
SQ  
Query Match 56.3%; Score 73.2; DB 6; Length 874;  
Best Local Similarity 77.1%; Pred. No. 4.1e-09;  
Matches 101; Conservative 0; Mismatches 29; Indels 1; Gaps 1;  
QY 1 TCCGCTACTCTCGGCTACCCCGGAAACCGCTTGCAGCTGGTGGCGGATGCC 60  
DB 341 TCCGCTACTCTCGGCTACCCCGGAAACCGCTTGCAGCTGGTGGCGGATGCC 400  
QY 61 GTGCTCTCCGACAGCCCGGCGCCGACCTGGGA-GNAGTGTGAGCGCTGTGACCTTGGCA 119  
DB 401 GTACTCTCCGACAGCCCGGCGCCGACCTGGGA-GNAGTGTGAGCGCTGTGACCTTGGCA 460  
QY 120 GGAAGCTGCT 130  
DB 461 AAAAGGCTACT 471

RESULT 8  
ABQ44402/C  
ID ABQ44402 standard; DNA; 874 BP.  
XX  
XX ABQ44402;  
AC  
XX 12-JUN-2002 (first entry)  
DT  
XX  
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 30993.  
DE  
XX  
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KM drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
XX SNP; cell differentiation; ds.  
XX  
XX Homo sapiens.  
OS

XX  
XX WO200218632-A2.  
PN  
XX 07-MAR-2002.  
PD  
XX  
XX 01-SEP-2001; 2001WO-EP010074.  
XX  
XX  
XX 01-SEP-2000; 2000DE-01043826.  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX WPI; 2002-371829/40.  
DR  
XX  
XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
XX Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
XX Sequence 874 BP; 119 A; 90 C; 291 G; 374 T; 0 U; 0 Other;  
SQ  
Query Match 56.3%; Score 73.2; DB 6; Length 874;  
Best Local Similarity 77.1%; Pred. No. 4.1e-09;  
Matches 101; Conservative 0; Mismatches 29; Indels 1; Gaps 1;  
QY 1 TCCGCTACTCTCGGCTACCCCGGAAACCGCTTGCAGCTGGTGGCGGATGCC 60  
DB 534 TCCGCTACTCTCGGCTACCCCGGAAACCGCTTGCAGCTGGTGGCGGATGCC 475  
QY 61 GTGCTCTCCGACAGCCCGGCGCCGACCTGGGA-GNAGTGTGAGCGCTGTGACCTTGGCA 119  
DB 474 GTACTCTCCGACAGCCCGGCGCCGACCTGGGA-GNAGTGTGAGCGCTGTGACCTTGGCA 415  
QY 120 GGAAGCTGCT 130  
DB 414 AAAAGGCTACT 404

RESULT 9  
ABQ44404  
ID ABQ44404 standard; DNA; 874 BP.  
XX  
XX ABQ44404;  
AC  
XX 12-JUN-2002 (first entry)  
DT  
XX  
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 30995.  
DE  
XX  
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KM

KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PE 01-SEP-2001; 2001WO-EP010074.  
XX  
PR 01-SEP-2000; 2000DE-01043826.  
XX  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
DR WPI; 2002-371829/40.  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (1i) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. AB013410-  
CC AB054121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
SQ Sequence 874 BP; 144 A; 90 C; 320 G; 320 T; 0 U; 0 Other;  
XX  
Query Match 47.7%; Score 62; DB 6; Length 874;  
Best Local Similarity 71.8%; Pred. No. 2.6e-06;  
Matches 94; Conservative 0; Mismatches 36; Indels 1; Gaps 1;  
XX  
OY 1 TCCGCTTACTCGGCTACCCCGGAAACCGCTTGCAGCTGTGGCGCTGATGGCGATTCC 60  
DB 341 TTCGTTATTTTCGGTTATTTTCGGGAATCGTTTCGAGTTGGCGCTGATGGCGATTTC 400  
OY 61 GTGCTCTCCGACAGCCCGGCCACCT-GGGAGNAGTGTGAGCGCTGTGACCTTGCA 119  
DB 401 GTGTTTTCGATGATTTTCGTTTATTTTGGGTAGAGTGTGACGTTGTAATTTCTGA 460  
OY 120 GGGACGCTGCT 130  
DB 461 GGGACGTTGTT 471  
XX  
RESULT 10  
ABO44405/C  
ID ABO44405 standard; DNA; 874 BP.  
XX  
AC ABO44405;  
XX

DT 12-JUL-2002 (first entry)  
XX  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 30996.  
XX  
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PE 01-SEP-2001; 2001WO-EP010074.  
XX  
PR 01-SEP-2000; 2000DE-01043826.  
XX  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
DR WPI; 2002-371829/40.  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (1i) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. AB013410-  
CC AB054121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
SQ Sequence 874 BP; 320 A; 320 C; 90 G; 144 T; 0 U; 0 Other;  
XX  
Query Match 47.7%; Score 62; DB 6; Length 874;  
Best Local Similarity 71.8%; Pred. No. 2.6e-06;  
Matches 94; Conservative 0; Mismatches 36; Indels 1; Gaps 1;  
XX  
OY 1 TCCGCTTACTCGGCTACCCCGGAAACCGCTTGCAGCTGTGGCGCTGATGGCGATTCC 60  
DB 534 TTCGTTATTTTCGGTTATTTTCGGGAATCGTTTCGAGTTGGCGCTGATGGCGATTTC 475  
OY 61 GTGCTCTCCGACAGCCCGGCCACCT-GGGAGNAGTGTGAGCGCTGTGACCTTGCA 119  
DB 474 GTGTTTTCGATGATTTTCGTTTATTTTGGGTAGAGTGTGACGTTGTAATTTCTGA 415  
OY 120 GGGACGCTGCT 130  
DB 414 GGGACGTTGTT 404  
XX  
RESULT 11

ADD34132  
 ID ADD34132 standard; DNA; 650 BP.  
 AC ADD34132;  
 DT 15-JAN-2004 (first entry)  
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1910.  
 XX  
 KM de; mouse; array; mitochondrial; hybridisation; energy-metabolism;  
 KM mitochondrial disease; oxidative phosphorylation dysfunction;  
 KM oxidative stress; apoptosis; aging.  
 XX  
 OS Mus musculus.  
 XX  
 PN W0203020220-A2.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 30-AUG-2002; 2002WO-US027886.  
 XX  
 PR 30-AUG-2001; 2001US-0316323P.  
 XX  
 PR 31-AUG-2001; 2001CA-02356540.  
 XX  
 PA (UYEM-) UNIV EMORY.  
 XX  
 PI Wallace DC, Levy S, Kerstam K, Procaccio V;  
 XX  
 DR WPI; 2003-300821/29.  
 XX  
 PT Array containing probes for genes involved in mitochondrial biology,  
 PT useful for determining mitochondrial biology gene expression profiles for  
 PT use in diagnosing pathologies and identifying biochemical pathways.  
 XX  
 PS Claim 2; SEQ ID NO 1910; 201pp; English.  
 XX  
 XX The invention relates to a novel array comprising at least two isolated  
 CC nucleotide molecules, each molecule having a sequence capable of uniquely  
 CC hybridising to a nucleic acid molecule which is an expression product of  
 CC a gene involved in mitochondrial biology. The array comprises two or more  
 CC isolated nucleic acid molecules or spots, each molecule having a sequence  
 CC chosen from sequence of 994 human probes and 2046 mouse probes. An array  
 CC of the invention is useful for determining an expression profile of a  
 CC mouse or human sample containing nucleic acid, by contacting the array  
 CC with the sample under conditions allowing selective hybridisation, and  
 CC measuring hybridisation of nucleic acid in the sample to the array to  
 CC produce an expression profile. The array is also useful for determining  
 CC an expression profile of a first labelled sample containing nucleic acid  
 CC relative to a second, differently labelled sample containing nucleic  
 CC acid. The second sample is a reference or a standard. An array is useful  
 CC for determining an expression profile diagnostic of an energy-metabolism-  
 CC related physiological condition. An array of the invention is useful for  
 CC determining mitochondrial biology gene expression profiles of organisms,  
 CC such as human, mice and closely related species, tissue and organs of  
 CC such organisms, which are useful for determining expression profiles  
 CC diagnostic of energy metabolism-related physiological conditions,  
 CC diagnosing such physiological conditions, identifying biochemical  
 CC pathways, genes, and mutations involved in such physiological conditions,  
 CC identifying therapeutic agents useful for preventing and/or treating such  
 CC physiological conditions, evaluating and/or monitoring the efficacy of  
 CC such therapies, and creating and identifying animal models of human  
 CC energy metabolism-related physiological conditions. An array is also  
 CC useful for defining expression signatures or profiles for mitochondrial  
 CC diseases, as well as distinguishing clinical disorders that result from  
 CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,  
 CC apoptosis and aging. An array of the invention contains probes of genes  
 CC not previously recognised to participate in mitochondrial biology. The  
 CC sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA  
 CC clones used to make the probes of the invention. Some sequences are not  
 CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,  
 CC 1906, 2408 and 2643.  
 XX  
 SQ Sequence 650 BP; 143 A; 172 C; 170 G; 165 T; 0 U; 0 Other;

Query Match 39.2%; Score 51; DB 10; Length 650;  
 Best Local Similarity 67.2%; Pred. No. 0.0014;  
 Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;  
 OY 1 TCCGCTTACCTCTGAGTACCCCGGAGACCGCTTTCAGTGTGTGGCGCTGATGCGGATTCC 60  
 DB 173 TCTCTCTTCTGCGAAGCCGGGCAATCGCTTGAGCTGTGGAAACAGATGCGAGATAG 232  
 OY 61 GTGCTCTCCGACAGCCCGGCGCCCACTGG-GAGNAGTGTGAGGCTGTGACTTTCGA 119  
 DB 233 TTGCTCTCCAAAGACCAAGACTTCACTGAGCGACCAACTGTGATGCTCTCGCTTCGG 292  
 OY 120 GGAGCGCT 127  
 DB 293 GGAGCGCT 300  
 RESULT 12  
 AAT33800/C  
 ID AAT33800 standard; cDNA to mRNA; 3288 BP.  
 AC AAT33800;  
 DT 05-DEC-1996 (first entry)  
 DE Murine interleukin-17 receptor cDNA.  
 XX  
 KM Interleukin-17 receptor; IL-17R; autoimmune disease; allergy; asthma;  
 KM graft rejection; inflammation; therapy; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 121..2715  
 FT /\*tag= a  
 FT sig\_peptide 121..213  
 FT /\*tag= b  
 FT mat\_peptide 214..2712  
 FT /\*tag= c  
 XX  
 PN W09629408-A1.  
 XX  
 PD 26-SEP-1996.  
 XX  
 PF 21-MAR-1996; 96WO-US004018.  
 XX  
 PR 23-MAR-1995; 95US-00410535.  
 XX  
 PR 07-AUG-1995; 95US-00538765.  
 XX  
 PA (IMMV) IMMUNEX CORP.  
 XX  
 PI Yao Z, Springs MK, Fanslow WC;  
 XX  
 DR WPI; 1996-443184/44.  
 DR P-PSDB; AAM04184.  
 XX  
 PT DNA encoding interleukin-17 receptor - useful for regulating immune and  
 PT inflammatory responses, or to suppress graft rejection.  
 XX  
 PS Claim 1; Page 25-29; 52pp; English.  
 XX  
 XX A cDNA clone (AAT33800) codes for murine interleukin-17 receptor (IL-17R)  
 CC (AAM04184), a type I transmembrane protein. A cDNA library of murine  
 CC thymoma B14 cells was used to transform CV1/EBNA cells and the prods.  
 CC were screened for binding to a fusion between the FC region of human IgG1  
 CC (see also AAM02305) and the viral IL-17 homologue HVS13 (AAM02387). A  
 CC positive clone contained a 3.2 kb insert that included the IL-17R open  
 CC reading frame. The cDNA can be used to produce (pref. soluble)  
 CC recombinant IL-17R in transformed host cells or to transfect a tissue or  
 CC organ as a means of suppressing graft rejection. It was also used to  
 CC identify a cDNA clone (AAT33801) coding for human IL-17R (AAM04185)

SQL Sequence 3288 BP; 733 A; 928 C; 906 G; 721 T; 0 U; 0 Other;

Query Match 28.3%; Score 36.8; DB 2; Length 3288;

Best Local Similarity 55.0%; Pred. No. 5.4;

Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

SQL Sequence 3288 BP; 733 A; 928 C; 906 G; 721 T; 0 U; 0 Other;

Query Match 28.3%; Score 36.8; DB 2; Length 3288;

Best Local Similarity 55.0%; Pred. No. 5.4;

Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

1 TCCGCTTACCTCGGCTACCCCGGAAACCGCTTGAAGTGTGACCTGATGCGGATTCC 60

2552 TCCCTCTCCGTGAGCCACTCGGGGGGCTGCGGGAGCTCTCGAGATGTAGCCCTGTGCC 2493

61 GTGCTCTCCGACAGCCCGGCGCCACCTGGAGNAGTGTGACCTCTGACCTTGGCAG 120

2492 GACTGCACCGACTGCGCTGCTCTCTCAGAGGTGTGACACCTCTCAGAGACCACTCT 2433

121 GGACGCTGC 129

2432 GGCTTCGCGC 2424

RESULT 13

AAV27591/c

AAV27591 standard; cDNA to mRNA; 3288 BP.

AAV27591;

12-OCT-1998 (first entry)

Mouse interleukin-17 receptor cDNA.

Interleukin-17 receptor; IL-17 receptor; mouse; nitric oxide; cartilage;

osteoarthritis; autoimmune disease; inflammation; therapy; ss.

Mus sp.

Key Location/Qualifiers

CDS 121..2715

sig\_peptide 121..213

mat\_peptide 214..2712

WO9823284-A1.

04-JUN-1998.

21-NOV-1997; 97WO-US021451.

27-NOV-1996; 96US-0052525P.

(IMMV ) IMMUNEX CORP.

Trout AB;

WPI; 1998-322457/28.

P-PSDB; AAW61271.

Reducing nitric oxide production by cartilage associated cells - by

contacting cells with soluble interleukin-17 receptor, useful to treat

osteoarthritis and auto-immune and inflammatory diseases.

Disclosure; Page 20-24; 41pp; English.

This cDNA sequence codes for mouse full-length interleukin-17 (IL-17)

receptor (see AAW61271). It can be used for the production of recombinant

IL-17 receptor polypeptides, especially a soluble polypeptide comprising

the signal peptide and extracellular domain of murine IL-17 receptor, in

prokaryotic or eukaryotic (for glycosylated products) expression systems.

A claimed method for reducing the amount of nitric oxide produced by a

cartilage associated cell comprises contacting the cell with a soluble IL

-17 receptor, especially soluble murine or human (see AAW61272) IL-17

receptor. IL-17 is known to stimulate nitric oxide production from

cartilage-associated cells in individuals with osteoarthritis. Inhibitors

of nitric oxide production, such as soluble IL-17 receptor, may therefore

be useful to ameliorate the effects of nitric oxide in osteoarthritis as

well as in other disease conditions in which nitric oxide plays a role,

e.g. autoimmune and inflammatory diseases

SQL Sequence 3288 BP; 733 A; 928 C; 906 G; 721 T; 0 U; 0 Other;

Query Match 28.3%; Score 36.8; DB 2; Length 3288;

Best Local Similarity 55.0%; Pred. No. 5.4;

Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

1 TCCGCTTACCTCGGCTACCCCGGAAACCGCTTGAAGTGTGACCTGATGCGGATTCC 60

2552 TCCCTCTCCGTGAGCCACTCGGGGGGCTGCGGGAGCTCTCGAGATGTAGCCCTGTGCC 2493

61 GTGCTCTCCGACAGCCCGGCGCCACCTGGAGNAGTGTGACCTCTGACCTTGGCAG 120

2492 GACTGCACCGACTGCGCTGCTCTCTCAGAGGTGTGACACCTCTCAGAGACCACTCT 2433

121 GGACGCTGC 129

2432 GGCTTCGCGC 2424

RESULT 14

AAV01921/c

AAV01921 standard; cDNA to mRNA; 3288 BP.

AAV01921;

21-APR-1999 (first entry)

Murine IL-17R cDNA.

IL-17R; murine; interleukin-17 receptor; immunoregulator; inhibitor;

T cell proliferation; T cell activation; organ graft; rejection;

autoimmune disease; allergy; asthma; treatment; inflammatory disease;

B cell proliferation; immunoglobulin secretion; immunogen; ss.

Mus sp.

Key Location/Qualifiers

CDS 121..2715

sig\_peptide 121..213

mat\_peptide 214..2712

US5869286-A.

09-FEB-1999.

21-MAR-1996; 96US-00620694.

23-MAR-1995; 95US-00410535.

07-AUG-1995; 95US-00538765.

(IMMV ) IMMUNEX CORP.

Spriggs MK, Fanelow WC, Yao Z;

WPI; 1999-152766/13.

P-PSDB; AAW92408.

Isolated interleukin-17 receptor DNA - used to develop products for

treating e.g. organ or graft rejection, autoimmune disease, allergy,

asthma or inflammatory disease.

Disclosure; Col 19-26; 25pp; English.

This sequence encodes a murine interleukin-17 receptor (IL-17R). IL-17R

polypeptides have immunoregulatory activity. They can be used for inhibiting T cell proliferation, or for inhibiting T cell activation. In particular they can be used for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. They can also be used for the prevention or treatment of inflammatory disease in which activated T cells play a role or for inhibiting B cell proliferation or immunoglobulin secretion. The IL-17 polypeptides can also be used as immunogens, reagents in in vitro assays, or as binding agents for affinity purification procedures

Sequence 3288 BP; 733 A; 928 C; 906 G; 721 T; 0 U; 0 Other;

Query Match 28.3%; Score 36.8; DB 2; Length 3288;  
Best Local Similarity 55.0%; Pred. No. 5.4; Mismatches 58; Indels 0; Gaps 0;  
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

1 TCCGCTTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGCGCTGATGCGGATTCC 60  
2552 TCCCTCTCCGAGAGCCACTCGGGGGGCTCGGGGAGCTCTGAGATGTAGCCCTGTGCC 2493

QY 61 GTGCTTCCGACAGCCCGGCCCCACCTGGAGAGNAGTGTACCGCTCGTACCTTCCGAG 120  
DB 2492 GACTGCACCGACTGCGCTGCTCTCTCCAGAGGGGTGTGACGCCCTCGAGAGACCACTCT 2433

QY 121 GGAGCGCTGC 129  
DB 2432 GGCTTCGGC 2424

RESULT 15  
AA51987/c  
ID AA51987 standard; cDNA to mRNA; 3288 BP.  
AC AA51987;  
XX  
XX 04-DEC-2000 (first entry)  
DT  
XX  
DE Murine interleukin-17 receptor coding sequence.  
XX  
XX IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;  
KM HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;  
KM anti-asthmatic; ss.  
XX  
OS Mus sp.  
XX  
XX Key Location/Qualifiers  
FH 121. .2715  
FT /\*tag= a  
FT /product= "IL-17\_receptor"  
FT sig\_peptide 121. .213  
FT /\*tag= b  
FT mat\_peptide 214. .2712  
FT /\*tag= c  
XX  
XX US6100235-A.  
XX  
XX 08-AUG-2000.  
XX  
XX 11-FEB-1998; 98US-00022260.  
XX  
XX 23-MAR-1995; 95US-00410535.  
XX 07-AUG-1995; 95US-00538765.  
XX 21-MAR-1996; 96US-00620694.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Farnlow WC, Spriggs MK, Yao Z;  
XX WPI; 2000-548298/50.  
XX P-PSDB; AAY97130.  
XX  
XX Regulating, treating or preventing immune or inflammatory response in a  
XX mammal, especially organ or graft rejection, allergy or asthma, comprises

PT administering interleukin-17 receptors.  
XX  
XX Example 2; Col 19-26; 26pp; English.  
PS  
XX A novel interleukin-17 receptor (IL-17R) was identified by screening a  
CC cDNA library from T cell thymoma EL4 cells, which were identified as  
CC binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc  
CC region and soluble IL-17 (CTLA-8) protein or a homologous Herpesvirus  
CC saimiri (HSV) protein, designated HSV13. Regulating an immune or  
CC inflammatory response in a mammal comprises administering soluble IL-17R.  
CC Soluble IL-17R fragments comprise residues 1-322 of the murine IL-17R,  
CC residues 1-320 of the human IL-17R, and fragments of the extracellular  
CC domain that bind IL-17. The method is useful for regulating an  
CC immunoreponse, for treating or preventing diseases like allergy, asthma  
CC and autoimmune diseases, and for suppressing rejection of grafted organs  
CC or tissues in the recipient

Sequence 3288 BP; 733 A; 928 C; 906 G; 721 T; 0 U; 0 Other;

Query Match 28.3%; Score 36.8; DB 3; Length 3288;  
Best Local Similarity 55.0%; Pred. No. 5.4; Mismatches 58; Indels 0; Gaps 0;  
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

1 TCCGCTTACCTCGGCTACCCCGGAAACCGCTTCGAGCTGTGCGCTGATGCGGATTCC 60  
2552 TCCCTCTCCGAGAGCCACTCGGGGGGCTCGGGGAGCTCTGAGATGTAGCCCTGTGCC 2493

QY 61 GTGCTTCCGACAGCCCGGCCCCACCTGGAGAGNAGTGTACCGCTCGTACCTTCCGAG 120  
DB 2492 GACTGCACCGACTGCGCTGCTCTCTCCAGAGGGGTGTGACGCCCTCGAGAGACCACTCT 2433

QY 121 GGAGCGCTGC 129  
DB 2432 GGCTTCGGC 2424

Search completed: June 7, 2005, 22:14:36  
Job time : 130.188 secs

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; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1221
; LENGTH: 28172
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-1221

Query Match      28.9%; Score 37.6; DB 4; Length 28172;
Best Local Similarity 56.0%; Pred. No. 0.43;
Matches 70; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 5 CCTACCTGCGTACCCGGGAAACGCTTCGAGCTGTGCGCTGATGGCGGATTCGGTGC 64
   |||||
Db 18175 CCGGTTACCCACGCGGACGCGCTTCGCGGCGCGCGCGCTTCGCTACTCGCGC 18234
   |||||
Qy 65 TCTCCGACAGCCCGCGCCCACTTGAGAGNAGTGCTGACGCTTCGACCTTCGACAGGAC 124
   |||||
Db 18235 CCAGTTTCATGAGCGCGCGCGCGCGCGAGATCTCTACACAGCGCGCTTCGAGAAC 18294
   |||||
Qy 125 GCTGC 129
   |||||
Db 18295 GCTGC 18299

RESULT 3
US-08-620-694A-1/c
; Sequence 1, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
; US-08-620-694A-1

Query Match      28.3%; Score 36.8; DB 2; Length 3288;
Best Local Similarity 55.0%; Pred. No. 0.54;
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1 TCCGCTACTCGGCTACCCCGGGAACCGCTTCGAGCTGTGCGCTGATGGCGGATTC 60
   |||||
Db 2552 TCTCTCTCCGTGACCACTCGGCGGCGCTGCGGAGGCTCTCGAGATGATACCTGTGTC 2493
   |||||
Qy 61 GTGCTTCCGACAGCCCGCGCCCACTTGAGAGNAGTGCTGAGCGCTGACCTTCGAG 120
   |||||
Db 2492 GACTGACCGACGCTCCGCTGCTCTCTCAAGGAGTGACGCTTCGAGACCACTCT 2433
   |||||
Qy 121 GAGCGTGC 129
   |||||
Db 2432 GCGCTCGGC 2424
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RESULT 4
US-09-022-255-1/c
; Sequence 1, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
US-09-022-255-1

Query Match 28.3%; Score 36.8; DB 3; Length 3288;

Best Local Similarity 55.0%; Pred. No. 0.54;

Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1 TCCGCTACCTCGGCTACCCCGGAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 60  
Db 2552 TCCTCTCTCCGTGAGCCACTCGGGGGGCTGCGGGAGCTCTGAGATGTAGCCCTGTGTC 2493  
Qy 61 GTGCTTCGACGAGCCCGGCGCCCACTGGAGAGNAGTGATGACGCTGTGACCTTGGCAG 120  
Db 2492 GACTGCACGACGACTGCGCTGCTCTCTCAAGAGGTGTGACAGCCCTCGAGACCACTCT 2433  
Qy 121 GGACGCTGC 129  
Db 2432 GGCTCTGGC 2424

## RESULT 5

US-09-022-696-1/C  
Sequence 1, Application US/09022696

Patent No. 6072037

GENERAL INFORMATION:

APPLICANT: Yao, Zhenbin

APPLICANT: Fanliow, William

TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,696

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
US-09-022-696-1

Query Match 28.3%; Score 36.8; DB 3; Length 3288;

Best Local Similarity 55.0%; Pred. No. 0.54;

Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1 TCCGCTACCTCGGCTACCCCGGAACCGCTTCGAGCTGTGGCGCTGATGCGGATTCC 60  
Db 2552 TCCTCTCTCCGTGAGCCACTCGGGGGGCTGCGGGAGCTCTGAGATGTAGCCCTGTGTC 2493  
Qy 61 GTGCTTCGACGAGCCCGGCGCCCACTGGAGAGNAGTGATGACGCTGTGACCTTGGCAG 120  
Db 2492 GACTGCACGACGACTGCGCTGCTCTCTCAAGAGGTGTGACAGCCCTCGAGACCACTCT 2433  
Qy 121 GGACGCTGC 129  
Db 2432 GGCTCTGGC 2424

## RESULT 6

US-08-978-773-1/C

Sequence 1, Application US/08978773

Patent No. 6083906

GENERAL INFORMATION:

APPLICANT: Trout, Anthony

TITLE OF INVENTION: Method of Regulating Nitric Oxide Production

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple PowerMacintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,773

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/052,525

FILING DATE: 27 NOVEMBER 1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2623-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3288 base pairs

TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
IMMEDIATE SOURCE:  
CLONE: IL-17 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2712  
US-08-978-773-1

Query Match 28.3%; Score 36.8; DB 3; Length 3288;  
Best Local Similarity 55.0%; Pred. No. 0.54;  
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1 TCCGCTTACCTCGGCTACCCCGGAAACCGCTTTCGAGCTGTGGCGCTGATGGCGGATTCC 60  
Db 2552 TCTCTCTCCGTGAGCCACTCGGGGGGGCTGGGGGAGCTCTCGAGATGATGAGCCCTGTCC 2493  
Qy 61 GTGCTCTCCGACAGCCCGGCCCCCACCCTGGAGAGNAGTGATGACCTCGTGAACCTTCCGAG 120  
Db 2492 GACTGCACCGACTGCGCGCTCTCTCTCAGAGGGGTGTGCAGCCCTCGAGGACCACTCT 2433  
Qy 121 GGACGCTGC 129  
Db 2432 GGCTCGGC 2424

## RESULT 7

US-09-022-253-1/c  
Sequence 1, Application US/09022253  
Patent No. 6096305

GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6096305e1 Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022.253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620.694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430

TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
US-09-022-253-1

Query Match 28.3%; Score 36.8; DB 3; Length 3288;  
Best Local Similarity 55.0%; Pred. No. 0.54;  
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1 TCCGCTTACCTCGGCTACCCCGGAAACCGCTTTCGAGCTGTGGCGCTGATGGCGGATTCC 60  
Db 2552 TCTCTCTCCGTGAGCCACTCGGGGGGGCTGGGGGAGCTCTCGAGATGATGAGCCCTGTCC 2493  
Qy 61 GTGCTCTCCGACAGCCCGGCCCCCACCCTGGAGAGNAGTGATGACCTCGTGAACCTTCCGAG 120  
Db 2492 GACTGCACCGACTGCGCGCTCTCTCTCAGAGGGGTGTGCAGCCCTCGAGGACCACTCT 2433  
Qy 121 GGACGCTGC 129  
Db 2432 GGCTCGGC 2424

## RESULT 8

US-09-022-260-1/c  
Sequence 1, Application US/09022260  
Patent No. 6100235

GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6100235e1 Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022.260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
US-09-022-260-1

Query Match 28.3%; Score 36.8; DB 3; Length 3288;  
Best Local Similarity 55.0%; Pred. No. 0.54;  
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1 TCCGCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGTGGCCGTGATGCC 60  
Db 2552 TCTCTCTCCGTGAGCACTCGGGGGGCTGCGGGAGCTCTGGAATGATGCTGATCC 2493  
Qy 61 GTGCTTCGACAGCCCGGCCCCACCTGGAGAGTGTAGCTGTGACCTTTCGAG 120  
Db 2492 GACTGCACCGACTGCGCTGCTCTCTCAAGAGGTGTGACGCTTCGAGACCACTCT 2433  
Qy 121 GGACGCTGC 129  
Db 2432 GGCTTCGGC 2424

RESULT 9  
US-09-022-259-1/c  
Sequence 1, Application US/09022259  
Patent No. 6191104  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanelow, William  
TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,259  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
US-09-022-259-1

Query Match 28.3%; Score 36.8; DB 3; Length 3288;  
Best Local Similarity 55.0%; Pred. No. 0.54;  
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1 TCCGCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGTGGCCGTGATGCC 60  
Db 2552 TCTCTCTCCGTGAGCACTCGGGGGGCTGCGGGAGCTCTGGAATGATGCTGATCC 2493  
Qy 61 GTGCTTCGACAGCCCGGCCCCACCTGGAGAGTGTAGCTGTGACCTTTCGAG 120  
Db 2492 GACTGCACCGACTGCGCTGCTCTCTCAAGAGGTGTGACGCTTCGAGACCACTCT 2433  
Qy 121 GGACGCTGC 129  
Db 2432 GGCTTCGGC 2424

RESULT 10  
US-09-022-257-1/c  
Sequence 1, Application US/09022257  
Patent No. 6197525  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanelow, William  
TITLE OF INVENTION: No. 6197525e1 Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,257  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
US-09-022-257-1

Query Match 28.3%; Score 36.8; DB 3; Length 3288;  
Best Local Similarity 55.0%; Pred. No. 0.54;  
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

OY 1 TCCGCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGTGGCCCTGATGGCGGATTCC 60  
DB 2552 TCCCTCTCCGAGACCTCGGAGGAGGCTCCGAGATGTAGCCCTGGTCC 2493  
OY 61 GTGCTCTCCGACAGCCCGGCGCCGACCTGGAGNAGTGATGACGCTCGTGAACCTTCCGAG 120  
DB 2492 GACTGCACCGACTGCGCGCTGCTCTCTCAGAGGGGTGTGACCCCTCGAGGACCACTCT 2433  
OY 121 GGACGCTGC 129  
DB 2432 GGCTCTCGGC 2424

RESULT 11  
US-09-549-679-1/c  
Sequence 1, Application US/09549679  
Patent No. 6680057  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
SPLIGGS, Melanie  
FANSLAW, William  
TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/549,679  
FILING DATE: 14-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE: <Unknown>  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-549-679-1

Query Match 28.3%; Score 36.8; DB 4; Length 3288;  
Best Local Similarity 55.0%; Pred. No. 0.54;  
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

OY 1 TCCGCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGTGGCCCTGATGGCGGATTCC 60  
DB 2552 TCCCTCTCCGAGACCTCGGAGGAGGCTCCGAGATGTAGCCCTGGTCC 2493  
OY 61 GTGCTCTCCGACAGCCCGGCGCCGACCTGGAGNAGTGATGACGCTCGTGAACCTTCCGAG 120  
DB 2492 GACTGCACCGACTGCGCGCTGCTCTCTCAGAGGGGTGTGACCCCTCGAGGACCACTCT 2433  
OY 121 GGACGCTGC 129  
DB 2432 GGCTCTCGGC 2424

RESULT 12  
US-09-902-540-6511  
Sequence 6511, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(1)5849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 6511  
LENGTH: 1482  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-6511

Query Match 26.2%; Score 34; DB 4; Length 1482;  
Best Local Similarity 57.0%; Pred. No. 2.8; Indels 46; Gaps 0;  
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

OY 3 CGCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGTGGCCCTGATGGCGGATTCC 62  
DB 1158 CGCGAGCTTCTCTCTTACCGGAGACGCTGTGAGCTGCGCGGTGGTGAAGACT 1217  
OY 63 GCTTCGACAGCCCGGCGCCGACCTGGAGNAGTGATGACGCTCT 109



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OM nucleic - nucleic search, using bw model

Run on: June 7, 2005, 06:21:09 ; Search time 122.203 Seconds

(without alignment)  
6090.078 Million cell updates/sec

Title: US-10-071-174A-37

Perfect score: 130

Sequence: 1 tccgcctactcgcgtacc.....acctcagagacgtcgt 130

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4285876 seqs, 2862396386 residues

Total number of hits satisfying chosen parameters: 8571752

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*

19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*

20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*

21: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

23: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*

24: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

25: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114.8	88.3	887	16	US-10-071-174-1
2	100.8	77.5	548	9	US-09-764-847-311
3	100.8	77.5	548	14	US-10-092-154-311
4	86.8	66.8	522	9	US-09-912-589-3
5	73.2	56.3	874	20	US-10-363-345A-30993
6	73.2	56.3	874	20	US-10-363-345A-30994
7	62	47.7	874	20	US-10-363-345A-30995
8	62	47.7	874	20	US-10-363-345A-30996

C	9	36.8	28.3	3288	19	US-10-742-161-1	Sequence 1, Appl1
C	10	36.8	28.3	3288	19	US-10-742-172-1	Sequence 1, Appl1
C	11	36.4	28.0	3630	19	US-10-437-963-12593	Sequence 12593, A
C	12	36.2	27.8	632	20	US-10-425-115-169387	Sequence 169387, A
C	13	36	27.7	486	15	US-10-156-761-1614	Sequence 1614, Ap
C	14	36	27.7	9025608	15	US-10-156-761-1	Sequence 1, Appl1
C	15	35.4	27.2	2412	17	US-10-260-238-1034	Sequence 1034, Ap
C	16	35.4	27.2	2959	19	US-10-437-963-62213	Sequence 62213, A
C	17	34.8	26.8	1783	19	US-10-437-963-54971	Sequence 54971, A
C	18	34.6	26.6	1095	19	US-10-437-963-93303	Sequence 93303, A
C	19	34	26.2	1595	18	US-10-424-599-103250	Sequence 103250, A
C	20	33.6	25.8	1077	17	US-10-260-238-313	Sequence 313, App
C	21	33.4	25.7	878	19	US-10-437-963-65205	Sequence 1406, Ap
C	22	33.4	25.7	878	19	US-10-437-963-65205	Sequence 65205, A
C	23	33	25.4	852	20	US-10-425-115-88641	Sequence 88641, A
C	24	33	25.4	1911	14	US-10-152-886-30	Sequence 88641, A
C	25	32.6	25.1	882	17	US-10-402-842-34	Sequence 30, Appl1
C	26	32.6	25.1	47988	17	US-10-402-842-1	Sequence 34, Appl1
C	27	32.4	24.9	385	15	US-10-767-701-28894	Sequence 1, Appl1
C	28	32.4	24.9	1194	15	US-10-156-761-3451	Sequence 28894, A
C	29	32.2	24.8	539	19	US-10-437-963-82849	Sequence 3451, Ap
C	30	32.2	24.8	1866	19	US-10-437-963-84852	Sequence 82849, A
C	31	32.2	24.8	17083	19	US-10-475-970-4	Sequence 84852, A
C	32	32	24.6	792	19	US-10-437-963-2791	Sequence 4, Appl1
C	33	32	24.6	877	20	US-10-437-963-171782	Sequence 2791, Ap
C	34	32	24.6	1489	19	US-10-437-963-22814	Sequence 171782, A
C	35	32	24.6	1786	20	US-10-739-930-5058	Sequence 22814, A
C	36	32	24.6	1806	20	US-10-739-930-5055	Sequence 5058, Ap
C	37	32	24.6	3807	17	US-10-282-122A-26053	Sequence 5055, Ap
C	38	31.8	24.5	993	19	US-10-437-963-10729	Sequence 26053, A
C	39	31.8	24.5	1010	10	US-09-735-056-29	Sequence 10729, A
C	40	31.8	24.5	2107	20	US-10-425-115-62599	Sequence 29, Appl1
C	41	31.6	24.3	560	18	US-10-424-599-55478	Sequence 62599, A
C	42	31.6	24.3	2079	15	US-10-156-761-1755	Sequence 55478, A
C	43	31.6	24.3	16018	9	US-09-764-869-1384	Sequence 1755, Ap
C	44	31.6	24.3	16018	14	US-10-091-504-1384	Sequence 1384, Ap
C	45	31.6	24.3	16018	17	US-10-227-577-1384	Sequence 1384, Ap

#### ALIGNMENTS

RESULT 1

US-10-071-174-1

Sequence 1, Application US/10071174

Publication No. US2003017671A1

GENERAL INFORMATION:

APPLICANT: REED, JOHN C.

APPLICANT: KE, NING

APPLICANT: GODZIK, ADAM

TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND

TITLE OF INVENTION: USING SAME

FILE REFERENCE: 087102-0272558

CURRENT APPLICATION NUMBER: US/10/071, 174

CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 60/267,166

PRIOR FILING DATE: 2001-02-07

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 887

TYPE: DNA

ORGANISM: Homo sapiens

US-10-071-174-1

Query Match: 88.3%, Score 114.8; DB 16; Length 887;

Best Local Similarity: 96.9%; Pred. No. 1.9e-25;

Matches 127; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

DB 242 TCCGCTACTCGGCTACCCCGGAGACCGCTTCAGCTGGTGGCGCTGATGCGGATTC 60

1 TCCGCTACTCGGCTACCCCGGAGACCGCTTCAGCTGGTGGCGCTGATGCGGATTC 60

1 TCCGCTACTCGGCTACCCCGGAGACCGCTTCAGCTGGTGGCGCTGATGCGGATTC 60

Qy	61	GTGCTCTCCGACAGCCCCGGCCCCACCT--GGAGANNAGTGATGACGCTCCGGACCTTGGCA	119
Db	302	GTGCTCTCCGACAGCCCCGGCCCCACCTGGGGGAGAGTGATGACGCTCCGGACCTTGGCA	361
Qy	120	GGGAGCGTCTCT	130
Db	362	GGGACGCTCTCT	372

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RESULT 2
US-09-764-847-311
; Sequence 311, Application US/09764847
; Patent No. US2002012767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 311
;
; LENGTH: 548

```

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1  FEATURE:
2  /
3  / NAME/KEY: SITE
4  / LOCATION: (16)
5  / OTHER INFORMATION: n equals a,t,g, or c
6  / NAME/KEY: SITE
7  / LOCATION: (20)
8  / OTHER INFORMATION: n equals a,t,g, or c
9  / NAME/KEY: SITE
10 / LOCATION: (26)
11 / OTHER INFORMATION: n equals a,t,g, or c
12 / NAME/KEY: SITE
13 / LOCATION: (28)
14 / OTHER INFORMATION: n equals a,t,g, or c
15 / NAME/KEY: SITE
16 / LOCATION: (53)
17 / OTHER INFORMATION: n equals a,t,g, or c
18 /
19 / US-09-764-847-311

```

Query Match	77.5%	Score 100.8	DB 9	Length 548
Best Local Similarity	92.9%	Pred. No. 3.5e-21		
Matches 105	Conservative	0	Mismatches 8	Indels 0
			Gaps	0
OY	18	CCCCGGGAAACGGCTTCGAGCTGATGCGCGCTGATGCGGATTC	CCGAGCTCTCCGACAGCC	77
Db	61	CCACGCGTCGGCTTCGAGCTGATGCGCGCTGATGCGGATTC	CCGAGCTCTCCGACAGCC	120
OY	78	CGGCCCCACTGGGAGNAGTGGTGAAGCTTCGATCGACGGAGCGCTGCT		130
Db	121	CGGCCCCACTGGGAGNAGTGGTGAAGCTTCGATCGACGGAGCGCTGCT		173

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RESULT 3
US-10-092-154-311
; Sequence 311, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed. - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 311
; LENGTH: 548
; TYPE: DNA
;

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? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (16)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (20)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (26)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (28)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (53)
? OTHER INFORMATION: n equals a,t,g, or c
US-10-092-154-311

```

Query Match	77.5%;	Score 100.8;	DB 14;	Length 548;
Best Local Similarity	92.9%;	Pred. No. 3.5e-21;		
Matches 105; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

QY 18 CCGCGGAAACGCGCTTCAGAGCTGATGGCGGTATGCGAGATTCCGAGCTCTCCGACAGGCC 77

Db 61 CCAAGCGTCCGCGCTTCAGAGCTGATGGCGGTATGCGAGATTCCGAGCTCTCCGACAGGCC 120

QY 78 CCGCGCCCACTTGGAGAGAAAGTGGTAAAGCTCTCGTGAACCTTCGAGAGGACAGCGTGCT 130

Db 121 CCGCGCCCACTTGGAGAGAGTGGTAAAGCTCTCGTGAACCTTCGAGAGGACAGCGTGCT 173

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US-09-912-599-3          RESULT 4
; US-09-912-599-3
; Sequence 3, Application US/09912599
; Patent No. US20020106731A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.,
; TITLE OF INVENTION: Bel-2-like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT044P1
; CURRENT APPLICATION NUMBER: US/09/912,599
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/03080
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/179,487
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/180,697
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-912-599-3

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	Query Match	Score	DB #	Length
Best Local Similarity	96.1%	Pred. No. 6.1e-17		
Matches	99	Conservative	0	Mismatches 3; Indels 1; Gaps 1;
QY	29	GCTTCGAGCTGTTGGCGCTGATGCGGATTCCTCCGACCTCCGACAGCGCCGAGCCCACT	88	
Db	1	GCTTCGACCTGATGGCGCTGATGGCGGATTCCTCCGACCTCCGACAGCGCCCGCCCACT	60	
QY	89	-GGAGNAGTGTGATCGCTCTGTAACCTTCGAGGAGCGCTCT	130	
Db	61	GGGGGAGAGTGTGATCGCTCTGTAACCTTCGAGGAGAGCGCTCT	103	

RESULT 5  
US-10-363-345A-30993/c  
; Sequence 30993, Application US/10363345A  
; Publication No. US20040234960A1

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; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30993
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-Island No: 30993
US-10-363-345A-30993
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Query Match          56.3%; Score 73.2; DB 20; Length 874;
Best Local Similarity 77.1%; Pred. No. 7.7e-13;
Matches 101; Conservative 0; Mismatches 29; Indels 1; Gaps 1;
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Oy 1 TCCGCTACTCTGGCTACCCCGGGAACCGCTTGCAGCTGTGCGCTGATGCGGATTCC 60
    |||
Db 534 TCCGCTACTCTGGCTACCCCGGGAACCGCTTGCAGCTGTGCGCTGATGCGGATTCC 475
Oy 61 GTGCTCTCCGACAGCCCCCGGCCCACTTGGA-GNAGTGTGACGCTGTGACCTTCCGA 119
    |||
Db 474 GTACTCTCCGACAGCCCCCGGCCCACTTAAACAAATATATACGCTGTGACCTTCCGA 415
Oy 120 GGGACGCTGCT 130
    |||
Db 414 AAAACGCTACT 404
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RESULT 6
US-10-363-345A-30994
; Sequence 30994, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30994
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-Island No: 30994
US-10-363-345A-30994
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Query Match          56.3%; Score 73.2; DB 20; Length 874;
Best Local Similarity 77.1%; Pred. No. 7.7e-13;
Matches 101; Conservative 0; Mismatches 29; Indels 1; Gaps 1;
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Oy 1 TCCGCTACTCTGGCTACCCCGGGAACCGCTTGCAGCTGTGCGCTGATGCGGATTCC 60
    |||
Db 341 TCCGCTACTCTGGCTACCCCGGGAACCGCTTGCAGCTGTGCGCTGATGCGGATTCC 400
Oy 61 GTGCTCTCCGACAGCCCCCGGCCCACTTGGA-GNAGTGTGACGCTGTGACCTTCCGA 119
    |||
Db 401 GTACTCTCCGACAGCCCCCGGCCCACTTAAACAAATATATACGCTGTGACCTTCCGA 460
Oy 120 GGGACGCTGCT 130
    |||
```

```
Db 461 AAAACGCTACT 471
```

```
RESULT 7
US-10-363-345A-30995
; Sequence 30995, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30995
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-Island No: 30995
US-10-363-345A-30995
```

```
Query Match          47.7%; Score 62; DB 20; Length 874;
Best Local Similarity 71.8%; Pred. No. 1.9e-09;
Matches 94; Conservative 0; Mismatches 36; Indels 1; Gaps 1;
```

```
Oy 1 TCCGCTACTCTGGCTACCCCGGGAACCGCTTGCAGCTGTGCGCTGATGCGGATTCC 60
    |||
Db 341 TTGCTTATTTTCGTTATTTTCGGAATCGTTTCAAGTTGGTGGCTGATGCGGATTTC 400
Oy 61 GTGCTCTCCGACAGCCCCCGGCCCACTT-GGAAGNAGTGTGACGCTGTGACCTTCCGA 119
    |||
Db 401 GTGTTTTCGATGATTTTCGTTTATTTTGGGTAGAGTGTGACGCTGTGATTTTCGTA 460
Oy 120 GGGACGCTGCT 130
    |||
Db 461 GGGACGTTGTT 471
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RESULT 8
US-10-363-345A-30996/c
; Sequence 30996, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30996
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-Island No: 30996
US-10-363-345A-30996
```

```
Query Match          47.7%; Score 62; DB 20; Length 874;
Best Local Similarity 71.8%; Pred. No. 1.9e-09;
Matches 94; Conservative 0; Mismatches 36; Indels 1; Gaps 1;
```

```
Oy 1 TCCGCTACTCTGGCTACCCCGGGAACCGCTTGCAGCTGTGCGCTGATGCGGATTCC 60
    |||
Db 534 TTGCTTATTTTCGTTATTTTCGGAATCGTTTCAAGTTGGTGGCTGATGCGGATTTC 475
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QY 1 TCCGCTACCTCGGCTACCCCGGAAACCGCTTCAGCTGTGTGGCCGTGATGGCGATTCC 60  
DB 2552 TCTCTCTCCGTGAGCCATCCGGGGGGCTGCGGGGAGCTCTGAGATGTAAGCCCTCGTCC 2493  
QY 61 GTGCTTCCGACAGCCCGGCGCCCACTGTGGAGNAGTGTGACGCTCTGTGACCTTCGAG 120  
DB 2492 GACTGACCGACGCTGCGCTGTGCTCTCTCAGAGGTGTGACGCTCTCGAGGACCACTCT 2433  
QY 121 GGACGCTGC 129  
DB 2432 GGCTTCGGC 2424

RESULT 11  
US-10-437-963-12593/c  
; Sequence 12593, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 12593  
; LENGTH: 3630  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_18706C.1  
US-10-437-963-12593

Query Match 28.0%; Score 36.4; DB 19; Length 3630;  
Best Local Similarity 55.1%; Pred. No. 0.095; Indels 0; Gaps 0;  
Matches 70; Conservative 0; Mismatches 57;

QY 3 CGCTACCTCGGCTACCCCGGAAACCGCTTCAGCTGTGTGGCCGTGATGGCGGATTCCGT 62  
DB 972 CGCCAGCGTCTCTGTCGCGCGGCAACCGGTTCCCGCGCGCGCTGCTCCCTCTC 913  
QY 63 GCTCTCCGACAGCCCGGCGCCCACTGTGGAGNAGTGTGACGCTGTGACCTTCGAGAG 122  
DB 912 GCCGACCGCGCGCGCGGCAACCGCTTCGCGGAGAAACCGCTTCGCGCGCGCGGAG 853  
QY 123 ACGCTGC 129  
DB 852 TCGCGGC 846

RESULT 12  
US-10-425-115-169387  
; Sequence 169387, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 169387  
; LENGTH: 632  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_86067C.1  
US-10-425-115-169387

Query Match 27.8%; Score 36.2; DB 20; Length 632;  
Best Local Similarity 55.7%; Pred. No. 0.13; Indels 0; Gaps 0;  
Matches 68; Conservative 0; Mismatches 54;

QY 9 CCGCTACCTACCCCGGAAACCGCTTCAGCTGTGTGGCCGTGATGGCGGATTCCGTCTTC 68  
DB 391 CCGCGCGCGGCAACCGCGGCACTGCGCTCTCTGCGGCGCTCGCGCGCGCGCTCGC 450  
QY 69 GCAAGCCCGGCGCCCACTGTGGAGNAGTGTGACGCTGTGACCTTCGAGAGAGCTG 128  
DB 451 CGCGCGCGCGCGCGCGCGCGCTGCTCGGGGAGCGCTGCGCGCGCTGCGCGGCTCGG 510  
QY 129 CT 130  
DB 511 CT 512

RESULT 13  
US-10-156-761-1614  
; Sequence 1614, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 1614  
; LENGTH: 486  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ..(486)  
US-10-156-761-1614

Query Match 27.7%; Score 36; DB 15; Length 486;  
Best Local Similarity 59.4%; Pred. No. 0.15; Indels 41; Gaps 0;  
Matches 60; Conservative 0; Mismatches 41;

QY 12 CGGCTACCCCGGAAACCGCTTCAGCTGTGTGGCCGTGATGGCGGATTCCGTCTTCGGA 71  
DB 345 CGGCTTCCCTCTGCGTGGTGGCGGCTCGGCTCTGTGCGCTGAGAGACGAGGCTGAGCGGA 404  
QY 72 CAGCCCGGCGCCCACTGTGGAGNAGTGTGACGCTCTGTGAC 112  
DB 405 CATCTCGCGCAGCTCTGCGCGGAGGCGGCTCGCGCGCGGAC 445

RESULT 14  
US-10-156-761-1/c  
; Sequence 1, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 1  
LENGTH: 9025608  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (4187715)  
OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-156-761-1

Query Match 27.7% Score 36; DB 15; Length 9025608;  
Best Local Similarity 59.4%; Pred. No. 0.066;  
Matches 60; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 12 CGGCTACCCCGGAAACCGCTTGAGCTGTGGCGCTGATGGCGGATTCGCTCTCCGA 71  
Db 1994191 CGGCTTCGCTGGGCGGGGTCGGCTCGTGGCGCTGGAGAGAGGCCGGAACCTGGCGGA 1994132  
Qy 72 CAGCCCCGCGCCACCTGGAGAGAGATGCTGACCGCTCTGAC 112  
Db 1994131 CATCTCGCGCACTCTCGCGGAGAGCGGCTCGGCCGAC 1994091

RESULT 15  
US-10-260-238-1034  
Sequence 1034, Application US/10260238  
Publication No. US20040016025A1  
GENERAL INFORMATION:  
APPLICANT: Budworth, Paul R.  
APPLICANT: Moughamer, Todd G.  
APPLICANT: Briggs, Steven P.  
APPLICANT: Cooper, Bret  
APPLICANT: Glazebrook, Jane  
APPLICANT: Goff, Stephen A.  
APPLICANT: Katagiri, Fumiyuki  
APPLICANT: Kreps, Joel  
APPLICANT: Provart, Nicholas  
APPLICANT: Rieke, Darrell  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
FILE REFERENCE: 60111-NP  
CURRENT APPLICATION NUMBER: US/10/260,238  
CURRENT FILING DATE: 2002-09-26  
PRIOR APPLICATION NUMBER: US 60/325,448  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/325,277  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/370,620  
PRIOR FILING DATE: 2002-04-04  
NUMBER OF SEQ ID NOS: 6077  
SEQ ID NO 1034  
LENGTH: 2412  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-10-260-238-1034

Query Match 27.2% Score 35.4; DB 17; Length 2412;

Best Local Similarity 60.6%; Pred. No. 0.2;  
Matches 57; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 3 CGCCTACCTGGCTAACCCCGGAAACCGCTTGAGCTGTGGCGCTGATGGGAGATTCGCT 62  
Db 1530 CCGGCTCGCGGCGAGAGAGCCCAACATCTTGGCGCGGCTTGAAGATGGAGCCGGGT 1589  
Qy 63 GCTCTCCGACAGCCCGGCGCCCACTGAGAGNAG 96  
Db 1590 GGTGACCTGAGCCCGGCTACCTGTGGAGCTG 1623

Search completed: June 7, 2005, 18:04:27  
Job time : 133.203 secs



and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

## ORIGIN

Query Match 99.2%; Score 129; DB 1; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-23;  
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTCCTGCTGCTACCCCGGGAACCGCTTCGAGCTGTGGCCCTGATGGCGATTCC 60  
 |||  
 Db 1 TCCGCTCCTGCTGCTACCCCGGGAACCGCTTCGAGCTGTGGCCCTGATGGCGATTCC 60  
 |||

QY 61 GTGCTCTCGACGAGCCCGGCGCCCACTCGAGAGAGTGTGACGCTTCGTGCGAG 120  
 |||  
 Db 61 GTGCTCTCGACGAGCCCGGCGCCCACTCGAGAGAGTGTGACGCTTCGTGCGAG 120  
 |||

QY 121 GGACGCTGCT 130  
 |||  
 Db 121 GGACGCTGCT 130  
 |||

RESULT 2  
 AA005293 206 bp mRNA linear EST 07-MAY-1997  
 LOCUS zh3tail.r1 Soares fetal liver spleen INFIS\_S1 Homo sapiens cDNA  
 DEFINITION clone IMAGE:428828 5', mRNA sequence.

ACCESSION AA005293  
 VERSION AA005293.1 GI:1448755  
 KEYWORDS EST.

ORGANISM Homo sapiens (human)  
 SOURCE Homo sapiens

REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Bonyfish; Osteichthyes; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 206)

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiappelli,B.,  
 Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,  
 Hashing,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,  
 Maris,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,  
 Rolfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,  
 Trevisan,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.  
 and Watta,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags  
 JOURNAL Genome Res. 6 (9), 807-828 (1996)  
 MEDLINE 97044478  
 PUBMED 8889549

## COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 849 Std Error: 0.00  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 126.

## FEATURES

source

1..206  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="CDB:1328597"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:428828"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares fetal liver spleen INFIS\_S1"  
 /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)  
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
 This is a subtracted version of the original Soares fetal  
 liver spleen INFIS library. 1st strand cDNA was primed  
 with a Pac I - oligo(dT) primer [5'

## ORIGIN

Query Match 57.2%; Score 74.4; DB 1; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 5.4e-09;  
 Matches 86; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 43 GCGGTGATGCGGATTCCTGCTCTCGACAGACCCCGCCCACTGCGG-AGNAGTGTG 101  
 |||  
 Db 1 GCGGTGATGCGGATTCCTGCTCTCGACAGACCCCGCCCACTGCGGATGAGTGTG 60  
 |||

QY 102 ACGCTCGTACCTTCGCGAGGAGCGTCT 130  
 |||  
 Db 61 ACGCTCGTACCTTCGCGAGGAGCGTCT 89  
 |||

RESULT 3  
 A1604990 339 bp mRNA linear EST 21-APR-1999  
 LOCUS v122b11.x1 Knowles Solter mouse unfertilized egg Mus musculus cDNA  
 DEFINITION clone IMAGE:836445 3', mRNA sequence.

ACCESSION A1604990  
 VERSION A1604990.1 GI:4614157  
 KEYWORDS EST.

ORGANISM Mus musculus (house mouse)  
 SOURCE Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 339)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,  
 Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuck,R.,  
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
 Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

TITLE Unpublished (1999)  
 JOURNAL

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:496661  
 This clone was previously sequenced on the 5' end only, this new  
 data is from the 3' end

Seq primer: Primer name ambiguous  
 High quality sequence stop: 319.

## FEATURES

source

1..339  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J x DBA/2J F1"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:836445"  
 /tissue\_type="unfertilized egg"  
 /lab\_host="DH10B"  
 /clone\_lib="Knowles Solter mouse unfertilized egg"  
 /note="Organ: unfertilized egg; Vector: pBluescribe  
 (modified); Site 1: MluI; Site 2: SalI; Cloned  
 unidirectionally from mRNA prepared from 5000 unfertilized  
 eggs. Primer: SalI (dT):  
 5'-CGGTGACCGTGCAGCTTTTCTTTTCTTTT-3'. cDNAs were  
 cloned into the MluI/SalI sites of a modified Bluescribe  
 vector using commercial linkers (NEB). Average insert  
 size: 1.0 Kb."

## ORIGIN

Query Match 39.2%; Score 51; DB 1; Length 339;  
Best Local Similarity 67.2%; Pred. No. 0.0054;  
Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

QY 1 TCCGCTACCTGCTACCCCGGGAACCGCTTCGAGCTGTGCGCGCTGATGCGGATTCC 60  
DB 54 TCTCTCTCTGCGAAGCCGGGGCAATGCCCTGAGCTGTGTAACAGATGCAAGTAAAG 113  
QY 61 GTGCTCTCGACAGACCGCCCGCCCACTTG-GAGNAGTGCTGACGCTGTAACCTTCGA 119  
DB 114 TTGCTCTCCAAAGACCAAGACTTCAGCTGAGCCCACTGTGATGCTCTCGGCTTCGCG 173  
QY 120 GGGAGCGT 127  
DB 174 GGGAGCGT 181

RESULT 4  
CA560084 448 bp mRNA linear EST 19-NOV-2002  
LOCUS K0267E03-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus  
DEFINITION musculus cDNA clone NIA:K0267E03 IMAGE:30051122 5', mRNA sequence.  
ACCESSION CA560084  
VERSION CA560084.1 GI:25104716  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 448)  
Piao Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A.,  
Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H.  
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library  
(Long)

JOURNAL Unpublished (2001)  
COMMENT Other ESTs: K0267E03-3  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
Plate: K0267 row: E column: 03  
Seq primer: M13 Reverse  
High quality sequence stop: 448  
POLYA=No.

FEATURES  
source location/Qualifiers

1..448  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="tae:K0267E03-5N"  
/db\_xref="taxon:10090"  
/clone="NIA:K0267E03 IMAGE:30051122"  
/tissue\_type="Unfertilized Egg"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Unfertilized Egg cDNA Library  
(Long)"  
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were  
extracted from a pool of 1488 unfertilized eggs.  
Double-stranded cDNAs were synthesized with an Oligo(dt)  
primer (Invitrogen):  
5'-pGACATGCTCTGATCGGAGCGCGCCCTTTTCTTTT-3',  
treated with T4 DNA polymerase, and purified by  
ethanol-precipitation. The cDNAs were ligated to  
lone-linker L1-Sal4, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using

Ex Tag polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.5 kb. The library was constructed  
by Yulan Piao (NIA)."

Query Match 39.2%; Score 51; DB 6; Length 448;  
Best Local Similarity 67.2%; Pred. No. 0.0054;  
Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

QY 1 TCCGCTACCTGCTACCCCGGGAACCGCTTCGAGCTGTGCGCGCTGATGCGGATTCC 60  
DB 133 TCTCTCTCTGCGAAGCCGGGGCAATGCCCTGAGCTGTGTAACAGATGCAAGTAAAG 192  
QY 61 GTGCTCTCGACAGACCGCCCGCCCACTTG-GAGNAGTGCTGACGCTGTAACCTTCGA 119  
DB 193 TTGCTCTCCAAAGACCAAGACTTCAGCTGAGCCCACTGTGATGCTCTCGGCTTCGCG 252  
QY 120 GGGAGCGT 127  
DB 253 GGGAGCGT 260

RESULT 5  
CA561864 478 bp mRNA linear EST 19-NOV-2002  
LOCUS K0293B04-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus  
DEFINITION musculus cDNA clone NIA:K0293B04 IMAGE:3005583 5', mRNA sequence.  
ACCESSION CA561864  
VERSION CA561864.1 GI:25106519  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 478)  
Piao Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A.,  
Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H.  
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library  
(Long)

JOURNAL Unpublished (2001)  
COMMENT Other ESTs: K0293B04-3  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
Plate: K0293 row: B column: 04  
Seq primer: M13 Reverse  
High quality sequence stop: 478  
POLYA=No.

FEATURES  
source location/Qualifiers

1..478  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="tae:K0293B04-5N"  
/db\_xref="taxon:10090"  
/clone="NIA:K0293B04 IMAGE:3005583"  
/tissue\_type="Unfertilized Egg"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Unfertilized Egg cDNA Library  
(Long)"  
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were

extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen): 5'-PGACTGATGCTAGATCGGAGGCGCCCTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

## ORIGIN

Query Match 39.2%; Score 51; DB 6; Length 478;

Best Local Similarity 67.2%; Pred. No. 0.0054; Mismatches 41; Indels 1; Gaps 1;

Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

QY 1 TCCGCTTACCTGCTACCCCGGAAACGCTTGCAGCTGTGCGCGTATGCGGATTCC 60  
DB 162 TCCCTCTTCTCGGAAGCCGGGCAATGCTGAGCTGTGAAACAGATGCGAGATAG 221  
QY 61 GTGCTTCCGACAGCCCGCCCACTTG-GAGNAGTGTGACGCTGTGACCTTGCA 119  
DB 222 TTGCTCTCCAAAGACCAAGACTTCACTGAGACCACTGTATGCTCTGCGCTTCGCG 281  
QY 120 GGGACGCT 127  
DB 282 GGGACGCT 289

RESULT 6 486 bp mRNA linear EST 11-MAR-1999  
LOCUS A1505208  
DEFINITION vq79g11.x1 Knowles Solter mouse 2 cell Mus musculus cDNA clone  
IMAGE:1108004 3', mRNA sequence.

ACCESSION A1505208  
VERSION A1505208.1 GI:4403059  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 486)  
AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Thelning, B., Allen, M., Bowers, Y.,  
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,  
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.

TITLE The WashU-NCI Mouse EST Project 1999  
JOURNAL Unpublished (1999)  
COMMENT Contact: Maria M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

FEATURES  
source Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL, contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:606172  
This clone was previously sequenced on the 5' end only, this new  
data is from the 3' end  
Seq primer: Primer name ambiguous  
High quality sequence stop: 485.  
Location/Qualifiers  
1..486  
/organism="Mus musculus"  
/mol\_type="mRNA"

/strain="C57BL/6J x DBA/2J F1"  
/db\_xref="taxon:10090"  
/clone="IMAG:1108004"  
/tissue\_type="embryo"  
/dev\_stage="2-cell"  
/lab\_host="DH10B"  
/clone\_lib="Knowles Solter mouse 2 cell"  
/note="Organ: embryo; Vector: Bluescribe (modified);  
Site 1: MluI; Site 2: SalI; Cloned unidirectionally from  
mRNA prepared from 13,500 2-cell stage embryos. Primer:  
SalI (dT): 5'-CGGTGACGTCGACCGCTTTT-3'. cDNAs  
were cloned into the MluI/SalI sites of a modified  
Bluescribe vector using commercial linkers (NEB).  
Average insert size: 1.2 kb."

## ORIGIN

Query Match 39.2%; Score 51; DB 1; Length 486;

Best Local Similarity 67.2%; Pred. No. 0.0054; Mismatches 41; Indels 1; Gaps 1;

Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

QY 1 TCCGCTTACCTGCTACCCCGGAAACGCTTGCAGCTGTGCGCGTATGCGGATTCC 60  
DB 283 TCCCTCTTCTCGGAAGCCGGGCAATGCTGAGCTGTGAAACAGATGCGAGATAG 342  
QY 61 GTGCTTCCGACAGCCCGCCCACTTG-GAGNAGTGTGACGCTGTGACCTTGCA 119  
DB 343 TTGCTCTCCAAAGACCAAGACTTCACTGAGACCACTGTATGCTCTGCGCTTCGCG 402  
QY 120 GGGACGCT 127  
DB 403 GGGACGCT 410

RESULT 7 524 bp mRNA linear EST 19-NOV-2002  
LOCUS K0274C06-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus  
musculus cDNA clone NIA:K0274C06 IMAGE:30051773 5', mRNA sequence.

ACCESSION CA560564  
VERSION CA560564.1 GI:25105219  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 524)  
AUTHORS Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Steag, C.A.,  
Martin, P., Alda, K., Tanaka, T. and Ko, M.S.H.  
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library  
(Long)

TITLE Unpublished (2001)  
JOURNAL Other ESTs: K0274C06-3  
COMMENT Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdaa@gsun.gsc.nia.nih.gov  
Plate: K0274 row: C column: 06  
Seq primer: M13 Reverse  
High quality sequence stop: 524  
POLY(A)=No.

FEATURES  
source Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="mRNA"

/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAG:1108004"  
/tissue\_type="embryo"  
/dev\_stage="2-cell"  
/lab\_host="DH10B"  
/clone\_lib="Knowles Solter mouse 2 cell"  
/note="Organ: embryo; Vector: Bluescribe (modified);  
Site 1: MluI; Site 2: SalI; Cloned unidirectionally from  
mRNA prepared from 13,500 2-cell stage embryos. Primer:  
SalI (dT): 5'-CGGTGACGTCGACCGCTTTT-3'. cDNAs  
were cloned into the MluI/SalI sites of a modified  
Bluescribe vector using commercial linkers (NEB).  
Average insert size: 1.2 kb."  
Location/Qualifiers  
1..524  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="NIA:K0274C06 IMAGE:30051773"  
/tissue\_type="Unfertilized Egg"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Unfertilized Egg cDNA Library  
(Long)"

/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://jgun.gsc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo (dt) primer (Invitrogen):  
5'-pGACTGATCTAGATCGGAGCGCGCCCTTTT-3',  
treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

## ORIGIN

Query Match 39.2%; Score 51; DB 6; Length 524;

Best Local Similarity 67.2%; Pred. No. 0.0054; Mismatches 41; Indels 1; Gaps 1;

Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

Qy 1 TCCGCTTACCTCGGCTACCCCGGGAACGCTTCGAGCTGTGGCCGTGATGCGGATTC 60  
Db 127 TCCCTCTTCTGCGAAGCCGGGGCAATCGCTCGAGCTGTGTAACAGATGCGAGTAA 186  
Qy 61 GTGCTCTCCGACAGCCCGCCGACCTGG-GAGNAGTGTGACGCTGTAACCTTCCGA 119  
Db 187 TTGCTCTCCAAAGCAAGACTTCACTGAGACCAACTGTGATCTCTGCGCTTCGCG 246  
Qy 120 GGGACGCT 127  
Db 247 GGGACGCT 254

RESULT 8  
CA557550 588 bp mRNA linear EST 19-NOV-2002  
LOCUS K0229B10-5N NIA Mouse Unfertilized Egg cDNA Library (long) Mus  
DEFINITION musculus cDNA clone NIA:K0229B10 IMAGE:30047445 5', mRNA sequence.  
ACCESSION CA557550  
VERSION CA557550.1 GI:25102015  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 588)  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Steggy, C.A., Martin, P., Alida, K., Tanaka, T. and Ko, M.S.H.  
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (long)

JOURNAL COMMENT  
unpublished (2001)  
Other ESTs: K0229B10-3  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: [cdna@jgun.gsc.nia.nih.gov](mailto:cdna@jgun.gsc.nia.nih.gov)  
Plate: K0229 row: B column: 10  
Seq primer: M13 Reverse  
High quality sequence stop: 588  
POLYA=No.

FEATURES  
SOURCE

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/mol\_type="mRNA"  
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/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://jgun.gsc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo (dt) primer (Invitrogen):  
5'-pGACTGATCTAGATCGGAGCGCGCCCTTTT-3',  
treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

## ORIGIN

Query Match 39.2%; Score 51; DB 6; Length 588;

Best Local Similarity 67.2%; Pred. No. 0.0054; Mismatches 41; Indels 1; Gaps 1;

Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

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Db 172 TCCCTCTTCTGCGAAGCCGGGGCAATCGCTCGAGCTGTGTAACAGATGCGAGTAA 231  
Qy 61 GTGCTCTCCGACAGCCCGCCGACCTGG-GAGNAGTGTGACGCTGTAACCTTCCGA 119  
Db 232 TTGCTCTCCAAAGCAAGACTTCACTGAGACCAACTGTGATCTCTGCGCTTCGCG 291  
Qy 120 GGGACGCT 127  
Db 292 GGGACGCT 299

RESULT 9  
BG080862 626 bp mRNA linear EST 17-DEC-2003  
LOCUS H3058C03-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone  
DEFINITION H3058C03 5', mRNA sequence.  
ACCESSION BG080862  
VERSION BG080862.2 GI:40014930  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 626)  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grabovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagata, R., Del, H., Wood, W.H., Becker, K.G. and Ko, M.S.H.

JOURNAL COMMENT  
embryo using a 15,000 mouse developmental cDNA microarray  
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)  
On Jan 26, 2001 this sequence version replaced gi:12563419.

Other ESTs: H3058C03-3  
 Contact: George J. Kargul  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@igsun.grc.nia.nih.gov  
 This clone set has been freely distributed to the community. Please  
 visit <http://1gsun.grc.nia.nih.gov/cdna/15k.html> for details.  
 Plate: H3058 row: C column: 03  
 Seq primer: -21M13 Reverse  
 High quality sequence stop: 626  
 POLYA=No.

## FEATURES

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 /lab\_host="DH10B"  
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 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

## ORIGIN

Query Match 39.2%; Score 51; DB 4; Length 626;  
 Best Local Similarity 67.2%; Pred. No. 0.0054;

Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

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174 TCCCTCTTCTGGAAGCCGGGCAATCGCTCGAGCTGTGAACAGATGGCAGATTAG 233
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|||||
234 TTGCTCTCCAAAGACCAAGACTTCGAGCTGTGAGCAACTGTATGTCTTGCGCTTCGCG 293
120 GGGAGCCT 127
|||||
294 GGGAGCCT 301

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## RESULT 10

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 ACCESSION CF915355  
 VERSION CF915355.1 GI:38186557  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

## REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

## COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 649)  
 Piao, Y., Ko, N.T., Lam, M.K. and Ko, M.S.H.  
 Construction of long-transcript enriched cDNA libraries from  
 submicrogram amounts of total RNAs by a universal PCR amplification  
 method  
 Genome Res. 11 (9), 1553-1558 (2001)  
 11544139  
 CONTACT: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@igsun.grc.nia.nih.gov  
 Plate: B0978 row: E column: 08  
 Seq primer: M13 Reverse  
 High quality sequence stop: 649  
 POLYA=No.

## FEATURES

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 /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://1gsun.grc.nia.nih.gov/cdna>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). (PMID: 11544139). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen): 5'-GGACTGAGTTCTAGATCGGAGCGCGCCCTTTT-3'), treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 39.2%; Score 51; DB 7; Length 649;  
 Best Local Similarity 67.2%; Pred. No. 0.0054;

Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

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1 TCCGCTTACCTGCTACCCCGGGAACCGCTTCGAGCTGTGGCGGTGCGGATTC 60
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174 TCCCTCTTCTGGAAGCCGGGCAATCGCTCGAGCTGTGAACAGATGGCAGATTAG 233
61 GTGCTCTCCGACAGCCCGGCCCACTGG-GAGNAGTGATGACGCTGTGACCTTGCGA 119
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234 TTGCTCTCCAAAGACCAAGACTTCGAGCTGTGAGCAACTGTATGTCTTGCGCTTCGCG 293
120 GGGAGCCT 127
|||||
294 GGGAGCCT 301

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RESULT 11  
BY735639  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

BY735639 736 bp mRNA linear EST 17-DEC-2002  
BY735639 RIKEN full-length enriched, 1 cell embryo Mus musculus  
cDNA clone 10C0031F16 5', mRNA sequence.  
BY735639  
BY735639.1 GI:27148766  
EST.  
Mus musculus  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 736)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
Batilov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,  
Chochoa, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
Flachner, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
Gariboldi, M., Glasi, C., Godzik, A., Gough, J., Grimmond, S.,  
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Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wyszewski, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carrinci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, U., Aizawa, K.,  
Aizawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Carrinci, P.,  
Fukuda, S., Hashizume, W., Hayashizaki, K., Hirozane, T., Hori, F.,  
Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
Nemura, K., Numazaki, R., Ohno, M., Otsu, N., Saito, R., Sakazume, N.,  
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,  
Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Computational Analysis of Full-length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

FEATURES  
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ORIGIN  
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Best Local Similarity 67.2% Pred. No. 0.0053;  
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185 TCCCTCTTCTCGGAAGCGCGGCGCATGCTCGAGCTGGGGAACAGATGCGAGTAAG 244  
61 GGGCTCTCGGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 119  
245 TTGCTCTCAAGACCAAGACTTTCAGCTGAGACCACTGATGATCTCTGCTTCCGG 304  
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DB 305 GGGAGCGCT 312

RESULT 12  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CO799635 758 bp mRNA linear EST 05-AUG-2004  
AGNCOURT 30246635 NIH MGC 256 Mus musculus cDNA clone  
IMAGE:30937853 5', mRNA sequence.  
CO799635  
CO799635.1 GI:50987815  
EST.  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 758)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: dsgerba@mail.nih.gov  
Tissue Procurement: Dr. Kathleen Horner, Stanford University  
cDNA Library Preparation: Express Genomics  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNLT at:  
<http://image.llnl.gov>  
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/note="Organ: oocyte; Vector: pExpress-1; Site: 1: EcoRV; Site 2: NotI; cDNA was primed using oligo-dT primer: 5'-pGACTAGTTCTAGATCGAGCGGCCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.2 kb. This is a primary library (normalized primary library is NIH\_MGC\_257) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH\_MGC library"

## ORIGIN

Query Match 39.2%; Score 51; DB 7; Length 758;  
Best Local Similarity 67.2%; Pred. No. 0.0053;  
Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

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207 TCTCTCTTCTGGAAAGCCGGGGCAATGCTGTGAGCTGTAACAGATGGCAATTAAG 266  
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61 GTGCTCTCCGACAGCCCGGCCCACTTG-GAGNAGGTGAGCGCTCGTGAACCTTGCA 119  
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267 TTGCTCTCAAGACCAAGACTTCACTGAGCCCAACTGTGATGCTCTGCGCTTCGCG 326  
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120 GGGACGCT 127  
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327 GGGACGCT 334

## RESULT 13

LOCUS

CO808612 763 bp mRNA linear EST 06-AUG-2004

DEFINITION AGENCOURT 30256728 NIH\_MGC\_256 Mus musculus cDNA clone

IMAGE:30938958 5', mRNA sequence.

CO808612

VERSION CO808612.1 GI:51025466

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 763)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics / NIH

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cga@bbs-r@mail.nih.gov

Tissue Procurement: Dr. Kathleen Horner, Stanford University

cDNA Library Preparation: Express Genomics

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence stop: 540.

Location/Qualifiers

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/note="Organ: oocyte; Vector: pExpress-1; Site: 1: EcoRV; Site 2: NotI; cDNA was primed using oligo-dT primer:

5'-pGACTAGTTCTAGATCGAGCGGCCGCC(T)25-3' and cloned into

the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb

resulted in an average insert size of 1.2 kb. This is a

primary library (normalized primary library is NIH\_MGC\_257)

and was constructed by Express Genomics (Frederick, MD).

Note: this is a NIH\_MGC library"

## ORIGIN

Query Match 39.2%; Score 51; DB 7; Length 763;  
Best Local Similarity 67.2%; Pred. No. 0.0053;  
Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

1 TCCGCTTACCTCGGCTACCCCGGAAACCGCTTCAGCTGTGGCGCTGATGGCGATTCC 60  
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72 TCTCTCTTCTGGAAAGCCGGGGCAATGCTGTGAGCTGTAACAGATGGCAATTAAG 131  
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61 GTGCTCTCCGACAGCCCGGCCCACTTG-GAGNAGGTGAGCGCTCGTGAACCTTGCA 119  
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120 GGGACGCT 127  
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192 GGGACGCT 199

## RESULT 14

LOCUS

CO797157 770 bp mRNA linear EST 05-AUG-2004

DEFINITION AGENCOURT 30256532 NIH\_MGC\_256 Mus musculus cDNA clone

IMAGE:30936954 5', mRNA sequence.

CO797157

VERSION CO797157.1 GI:50985337

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 770)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics / NIH

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cga@bbs-r@mail.nih.gov

Tissue Procurement: Dr. Kathleen Horner, Stanford University

cDNA Library Preparation: Express Genomics

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM1193 row: h column: 19

High quality sequence start: 23

High quality sequence stop: 417.

Location/Qualifiers

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/lab\_host="DH10B Tona"

/clone\_1lb="NIH\_MGC\_256"

/note="Organ: oocyte; Vector: pExpress-1; Site: 1: EcoRV; Site 2: NotI; cDNA was primed using oligo-dT primer:

5'-pGACTAGTTCTAGATCGAGCGGCCGCC(T)25-3' and cloned into

the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb

resulted in an average insert size of 1.2 kb. This is a

primary library (normalized primary library is NIH\_MGC\_257)

and was constructed by Express Genomics (Frederick, MD).

## ORIGIN

Query Match 39.2%; Score 51; DB 7; Length 770;  
Best Local Similarity 67.2%; Pred. No. 0.0053;  
Matches 86; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

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Qy      120 GGGACGCT 127
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Job time : 794.354 secs

## RESULT 15

CO814648

LOCUS

DEFINITION CO814648 772 bp mRNA linear EST 06-AUG-2004

IMAGE:30937746 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CO814648 772 bp mRNA linear EST 06-AUG-2004  
AGENCOURT\_30246837 NIH\_MGC\_256 Mus musculus cDNA clone  
IMAGE:30937746 5', mRNA sequence.  
CO814648  
CO814648.1 GI:51033274  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1. (bases 1 to 772)  
NIH-MGC <http://mgs.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Kathleen Horner, Stanford University  
cDNA Library Preparation: Express Genomics  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: NDAM1195 row: 1 column: 19  
High quality sequence start: 5  
High quality sequence stop: 666.  
Location/Qualifiers  
1.772  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30937746"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_256"  
/note="Organ: oocyte; Vector: pExpress-1; Site\_1: EcoRV;  
Site\_2: NotI; cDNA was primed using oligo-dT primer:  
5'-pGACTGATCTTAGATCGAGCGGCCCT(T)25-3' and cloned into  
the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb  
resulted in an average insert size of 1.2 kb. This is a  
primary library (normalized primary library is NIH\_MGC\_257)  
and was constructed by Express Genomics (Frederick, MD).  
Note: this is a NIH\_MGC library"

## FEATURES

source

1.772  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30937746"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_256"  
/note="Organ: oocyte; Vector: pExpress-1; Site\_1: EcoRV;  
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## ORIGIN

Query Match 39.2%; Score 51; DB 7; Length 772;

Best Local Similarity 67.2%; Pred. No. 0.0053; Mismatches 41; Indels 1; Gaps 1;

Matches 86; Conservative 0;

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Qy      1 TCGCCTTACCTCGGCTACCCCGGGAACCGCTTGAAGCTGAGCGGTGAGGAGATTC 60
Db      198 TCCTCTTCTGCGAAGCCCGGCGCAATCGCTGAGCTGTGAACAGATGGCAGTAAG 257
Qy      61 GTGCTCTCGACAGACCCCGCCGCTGAG-6AGNAGTGTGACGCTCGGACTTCGCA 119
Db      258 TTGCTCTCCAAAGACCAGACTTCAGCTGAGCCCACTGTGTGCTCTCGGCTTCGCG 317

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